

**Improving microbial fate and transport modeling to support TMDL development in an
urban watershed**

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ABSTRACT

Pathogen contamination, typically quantified by elevated levels of fecal indicator bacteria (FIB), remains the leading cause of surface water-quality impairments in the United States. Continuous watershed-scale models are typically employed to facilitate Total Maximum Daily Load (TMDL) restoration efforts. Due to limited understanding of microbial fate and transport, predictions of FIB concentrations are associated with considerable uncertainty relative to other water-quality contaminants. By focusing on a data-rich instrumented urban watershed, this study aims to improve understanding of microbial fate and transport processes. Weekly FIB concentrations in both the water column and streambed sediments were monitored for one year, and statistical correlations with hydrometeorological and physicochemical variables were identified. An intensive six storm intra-sampling campaign quantified and contrasted loading trends of both traditional regulatory FIB and emerging Microbial Source Tracking (MST) markers. Together, these intensive monitoring efforts facilitated evaluation of the impacts of bacteria-sediment interactions on the predictions of daily FIB concentrations in Hydrological Simulation Program-Fortran (HSPF) over multiple years. While superior overall model performance was demonstrated as compared to earlier efforts, the inclusion of bacteria-sediment interactions did not improve performance. Large wet-weather microbial loading appears to have dwarfed the effects of FIB

release and resuspension from sediment. Although wet-weather loading is generally considered as a primary source of waterbody microbial loads, dry-weather periods are more directly associated with public health concern, which may be a more suitable area for future model-refinement efforts. Site evaluation is critical to determine whether the added model complexity and effort associated with partitioning phases of FIB can be sufficiently offset by gains in predictive capacity. Finally, a stochastic framework to translate simulated daily FIB concentrations into estimates of human illness risks is presented that can be readily integrated into existing TMDLs. As even small concentrations of FIB from human sources are associated with great risk, and monitoring efforts indicated moderate/high levels of human-associated MST marker in this watershed, remediation efforts to protect public health would be best directed toward infrastructure improvements. Uncertainty analysis indicates more site-specific knowledge of pathogen presence and densities would best improve the estimation of illness risks.

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Chapter 1. Introduction

1.1. Study Justification

Microbial water-quality degradation is a global public health concern (Ford and Colwell, 1996, Hyer and Mayer, 2004, Coffey et al., 2010, WASH, 2012). In the past several decades, continued waterborne outbreaks, even in developed nations, have spurred extensive cooperation among experts from diverse fields – including hydrology, microbiology, engineering, epidemiology, medicine, and risk assessment - to better design strategies to protect and/or remediate source waters (Ford and Colwell, 1996, Lechevallier and Buckley, 2007, APEC, 2012). Nevertheless, exposure to pathogenic microorganisms via contaminated waters remains responsible for at least 40,000 cases of contagious disease annually at a direct healthcare cost of \$970 million in the United States alone (Collier et al., 2012).

Pathogens contamination, typically identified via elevated levels of fecal indicator bacteria (FIB), remains the leading cause of surface water-quality impairments in the United States (USEPA, 2015). Under the 1972 Clean Water Act, states are required to address identified impairments through the development of Total Maximum Daily Load (TMDL) restoration plans. Due to the technical difficulties and considerable expense associated with the continuous monitoring of FIB, water-quality models are commonly used in the TMDL process to identify the relative contributions of potential watershed sources of FIB and to evaluate the effectiveness of proposed restoration plans (NRC, 2001, Benham et al., 2006). The ability to develop robust and effective TMDLs is therefore directly dependent on the quality of models. Unfortunately, model simulations of microbial fate and transport are notoriously plagued by uncertainty (Novotny, 2003, Benham et

al., 2006, Benham et al., 2011). Bacteria are most commonly represented as “free” or dissolved-phase contaminants with near-neutral buoyancy in existing models, although a growing number of studies indicate that the re-suspension of particle-associated cells from bottom sediments can be an important source of water column bacteria concentrations (Bai and Lung, 2005, Jamieson et al., 2005, Fries et al., 2006, Krometis et al., 2009, Rehmann and Soupir, 2009, Cho et al., 2010, Pandey et al., 2012). Bacteria associated with sediments may also survive longer in the environment and potentially pose human health risks for an extended period of time (Droppo et al., 2009). A quantitative understanding of the impacts of sediments on bacteria fate and transport in receiving waters would significantly advance modeling capabilities, and thus promote effective TMDL development. Implementation of these environmental processes within existing models is currently limited by the lack of observational water-quality information for model development, calibration and validation.

While TMDL development represents a significant investment of financial resources (e.g. Birkeland (2001) estimated costs run from roughly 4,000 to 1,000,000 dollars per TMDL developed), it is unclear whether numerical compliance with FIB-based water-quality standards is an effective and efficient method to protect public health. Previous studies have indicated that the absence of FIB in water does not ensure the absence of pathogens and, conversely, that their presence does not always correlate with public health risk (Wu et al., 2011). This deficiency is partly attributed to the inherent difficulty in using FIB as an approximation for the presence of all pathogens. Although the presence of *E. coli* and enterococci generally indicates fecal contamination of a water body, previous studies indicate these bacteria are poorly correlated to the detection of many pathogenic microorganisms (e.g. *Salmonella* spp., *Campylobacter* spp.,

Cryptosporidium and *Giardia* spp, and human enteroviruses) (Harwood et al., 2005, Field and Samadpour, 2007, Yates, 2007, Wu et al., 2011). In addition, though most models consider fecal loads from a wide range of different sources during TMDL development, a single total FIB concentration is ultimately returned to compare with the applicable standards established based on epidemiological studies at human-sewage dominated coastal waters (USEPA, 2012). Previous risk assessments based on existing knowledge of pathogen presence and dose-response models indicate that risk varies widely by source. While it is generally accepted that the most serious threat to human health is from human fecal contamination rather than from animals (Field and Samadpour, 2007, Benham et al., 2011), fresh cattle feces can sometimes pose comparable human gastrointestinal illness risks to that from human sources due to the presence of zoonotic pathogens (Soller et al., 2010). At present, it is therefore difficult to assess the health risks related to different proposed watershed restoration plans to address high FIB concentration, which can lead to confusion for stakeholders participating in the process (Keller and Cavallaro, 2008).

Quantitative Microbial Risk Assessment (QMRA) modeling is a mathematical strategy used to link environmental exposure to illness risk via existing epidemiological relationships. Four major steps are generally employed in the risk assessment process: 1) hazard identification, which involves the documentation of all health effects associated with a particular pollutant; 2) dose-response assessment, which characterizes the relationship between dose amounts and the incidence of adverse health effects; 3) exposure assessment, which is used to determine the demographics of the exposed population as well as the route, amount, and duration of exposure to a particular pollutant; and 4) risk characterization, which involves the integration of the exposure, dose-response, and hazard identification steps in order to develop an estimate of the magnitude of the

impact from an environmental hazard (Haas et al., 2014). Previous studies have demonstrated the capability of QMRA to link single measures of FIB or pathogen concentrations to public health risks in recreational waters (Ashbolt et al., 2010, Schoen and Ashbolt, 2010, Soller et al., 2010, Soller et al., 2010, USEPA, 2010, Tserendorj et al., 2011, McBride et al., 2013). Most studies, however, were done under idealized conditions and failed to account for bacteria fate and transport processes (Ashbolt et al., 2010, Schoen and Ashbolt, 2010, Soller et al., 2010, USEPA, 2010, Veldhuis et al., 2010, Schmidt and Emelko, 2011, McBride et al., 2013). Temporal or climatic variations of bacteria loading in receiving waters are therefore not well captured. Linking QMRA with a fate and transport model would allow for a holistic evaluation of water-quality impairments and provide greater clarity in prioritizing restoration efforts during TMDL development and implementation planning.

1.2. Goal and Objectives

The overall goal of this study is to improve current understanding of microbial fate and transport processes, which will facilitate the development of a framework to translate *E. coli* concentrations as existing TMDL endpoints to human health risks. Specific objectives include:

- 1) Statistically identify potential correlations between water and sediment FIB (i.e. *E. coli* and enterococci) concentrations with available environmental variables following establishment of a weekly FIB monitoring regimen;
- 2) Investigate intra-and inter-storm patterns of loads of culturable and molecular fecal indicators;

- 3) Evaluate the long-term impacts of sediment on the prediction of FIB concentrations in HSPF by augmenting the existing model with a bacteria-sediment association module; and
- 4) Estimate source-specific and total human illness risks through linking HSPF outputs to a stochastic QMRA model.

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Chapter 2. Hydrometeorological and physicochemical drivers of fecal indicator bacteria in an urban stream bottom sediments

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Abstract

High levels of fecal indicator bacteria (FIB) are the leading cause of surface water-quality impairments in the United States. Watershed-scale models are commonly used to identify relative contributions of watershed sources and to evaluate the effectiveness of remediation strategies. However, most existing models simplify FIB transport behavior as equivalent to that of dissolved-phase contaminants, ignoring the impacts of sediment on the fate and transport of FIB. Implementation of sediment-related processes within existing models is limited by minimal available monitoring data on sediment FIB concentrations for model development, calibration, and validation purposes. The purpose of the present study is to evaluate FIB levels in the streambed sediments as compared to those in the water column and to identify environmental variables that influence water and underlying sediment FIB levels. Concentrations of *E. coli* and enterococci in the water column and sediments of an urban stream were monitored weekly for one year, and correlated with a variety of potential hydrometeorological and physicochemical variables. Increased FIB concentrations in both the water column and sediments were most strongly correlated with increased antecedent 24-h rainfall, increased stream water temperature, decreased dissolved oxygen, and decreased specific conductivity. These observations will support future efforts to incorporate sediment-related processes in existing models through the identification of key FIB relationships with other model inputs, and the provision of sediment FIB concentrations for direct model calibration. In addition, identified key variables can be used in quick evaluation of the effectiveness of potential remediation strategies.

2.1. Introduction

Elevated levels of fecal indicator bacteria (FIB) are the leading cause of surface water-quality impairments in the United States (USEPA, 2012a). Under the 1972 Clean Water Act, states are required to address identified impairments through the development of basin-specific Total Maximum Daily Load (TMDL) restoration plans. A TMDL is a “pollutant budget” that quantifies the maximum loadings of a contaminant that a waterbody can receive while still safely meeting applicable water-quality standard (USEPA, 2012a). Due to the technical difficulties and considerable expense associated with monitoring FIB levels, water-quality models are commonly used in the TMDL process to estimate the relative contributions of various watershed sources of FIB and to evaluate the effectiveness of potential load-reduction strategies. The ability to develop robust and effective TMDLs is therefore directly dependent on model accuracy. However, efforts to model FIB fate and transport are notoriously plagued by uncertainty, largely associated with current limitations in understanding the relative importance of various microbial behaviors in receiving waters (Benham et al., 2006; Shirmohammadi et al., 2006).

In most existing microbial water-quality models, FIB are assumed to behave in a manner similar to dissolved-phase contaminants (Jamieson et al., 2004). However, an increasing number of laboratory and field-scale studies suggest that FIB fate and transport is much more complex (Fig. 2-1). For example, a significant fraction of waterborne bacteria are associated with settleable particulates in stream sediments, which can be re-suspended into the water column if subsequently disturbed (Jamieson et al., 2005b; Krometis et al., 2009b; Rehmann and Soupir, 2009). Bacteria associated with particulates can persist in the environment and may pose human health risks for

an extended period of time (Droppo et al., 2009), further emphasizing the need to consider sediment-related processes in modeling in-stream FIB concentrations.

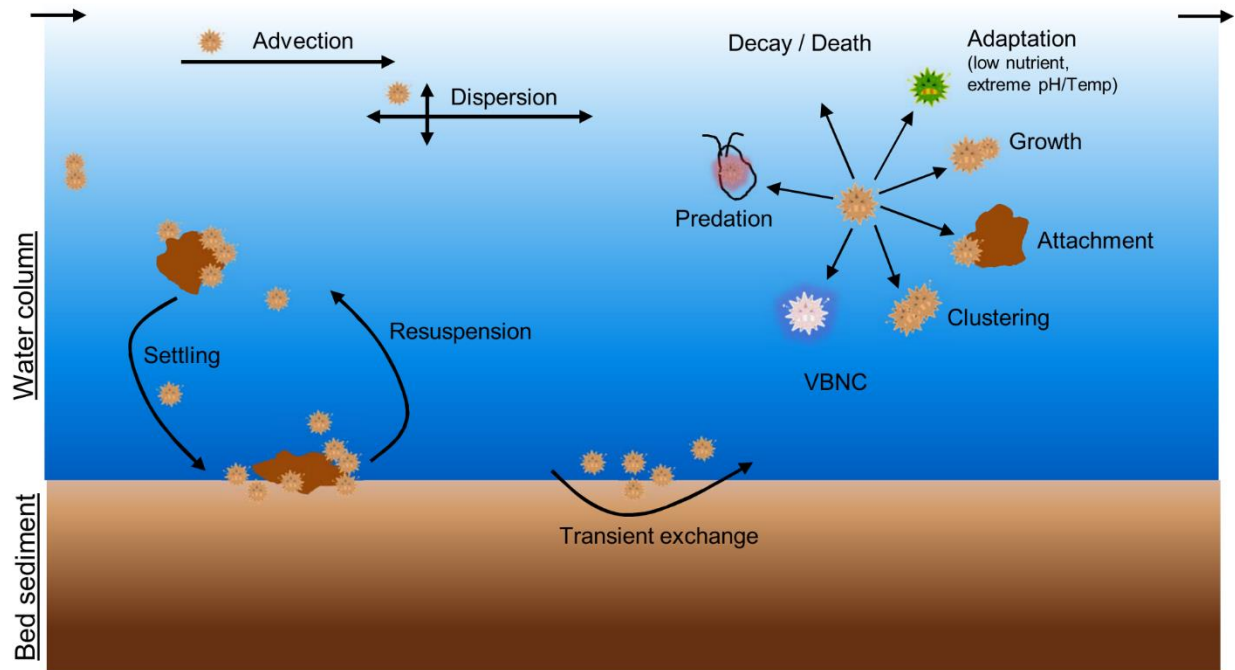


Figure 2-1. Major in-stream bacterial fate and transport processes. Current watershed-scale models generally only account for advection, dispersion, and first-order decay, although several studies have developed models by including other fate and transport processes (Kim et al., 2010; Russo et al., 2011; Wilkinson et al., 2011). VBNC = viable but not culturable.

In order to better understand the dynamics of FIB fate and transport, several previous studies have used existing water-quality monitoring datasets to correlate environmental variables and FIB concentrations in the water column. These studies largely associated water FIB levels with measures of precipitation in watersheds, i.e. rainfall/antecedent rainfall generally appear positively correlated with FIB concentrations (Mallin et al., 2001; Reeves et al., 2004; Gentry et al., 2006; Vidon et al., 2008; Hathaway et al., 2010). This is not surprising, as many studies have noted that increases in water FIB concentrations were associated with runoff-generating storm events

(Gaffield et al., 2003; Krometis et al., 2007b). A separate study of two Midwestern watersheds observed a significant positive relationship between water FIB concentrations and average daily discharge (Vidon et al., 2008), which may reflect the “flushing” of sediment associated FIB concentrations. With respect to related water-quality metric, increases in turbidity have been correlated with increases in water FIB concentrations in both coastal (Mallin et al., 2001) and inland waters (Gentry et al., 2006; Vidon et al., 2008; Huey and Meyer, 2010). While total suspended solids (TSS) concentrations have been positively correlated with water FIB concentrations in several studies of inland freshwaters (McCarthy et al., 2007; Huey and Meyer, 2010), no statistical significant correlations were observed between TSS and water FIB concentrations in a study of the Neuse River Estuary by Fries et al. (2006). This may reflect the existence of different relationships between FIB and TSS in different types of watershed or geographic region.

Unlike water column levels of FIB, FIB concentrations in natural streambed sediments are not typically monitored by environmental agencies. Available datasets for the development of models incorporating fluxes of microorganisms between the water column and sediments are therefore quite limited. Previous efforts to incorporate sediment-related processes in modeling in-stream FIB concentrations have relied on theoretical estimates or very limited streambed FIB monitoring data for model formulation, calibration or validation purposes, which introduced considerable uncertainty (Bai and Lung, 2005; Pandey et al., 2011; Russo et al., 2011).

The overall goal of this study is to improve the current understanding of patterns of FIB concentrations in streambed sediments, and to inform future monitoring efforts and subsequent

model development. This effort focuses on an impaired stream within a highly urbanized watershed in the Virginia Ridge and Valley ecoregion, where TMDL development is required by the Virginia Department of Environment Quality (VADEQ) under the U.S Clean Water Act sections 305(b) and 303(d). Specific objectives include 1) quantification and comparison of water and sediment FIB concentrations; and 2) identification of key hydrometeorological and physicochemical water-quality variables associated with FIB levels in the water column and streambed sediments. To our best knowledge, this is the first study investigating correlations between sediment FIB concentrations and other environmental variables. As many microbial fate and transport processes are difficult to measure in natural conditions but are highly coupled to a variety of more readily measurable hydrometeorological and physicochemical factors (Vidon et al., 2008), identifying the dominant factors influencing FIB levels in both the water column and underlying sediments of receiving waters will assist with incorporation of sediment-related processes in model development.

2.2. Materials and methods

2.2.1. Study area description

The present study is centered within the Virginia Tech StREAM Lab (Stream Research, Education, And Management) along Stroubles Creek in Blacksburg, VA (<http://www.bse.vt.edu/site/streamlab/>; Figure 2-2). Stroubles Creek flows approximately 15 km from northeastern Blacksburg, through the Virginia Tech campus, and into the New River, which has served as the region's main source of drinking water supply and home to a variety of recreational activities since the early 1950s (Parece et al., 2010). The 62-km² watershed is within the Ridge and Valley ecoregion, which is characterized by dolomite and limestone formations with

numerous sinkholes and natural springs. The streambed is composed of alluvial-floodplain deposits of stratified unconsolidated silt, clay and sand with lenses and beds of cobbles and pebbles (Parece et al., 2010). A TMDL to address high sediment loads impacting stream benthic macroinvertebrate communities were developed for the stream in the early 2000s (VADEQ and VADCR, 2003, VADEQ and VADCR, 2006). The 10-km benthic-impaired segment draining the highly urbanized Upper Stroubles Creek watershed (approximately 50% residential; 34% impervious surfaces) is also impaired by fecal contamination indicated by elevated *E. coli* concentrations. The benthic TMDL assumed that microbial loadings would also be substantially reduced through sediment control practices, as past experimental and field studies have reported significant associations between suspended sediments and indicator organisms (Ling et al., 2002; Jeng et al., 2005; Cizek et al., 2008; Krometis et al., 2010).

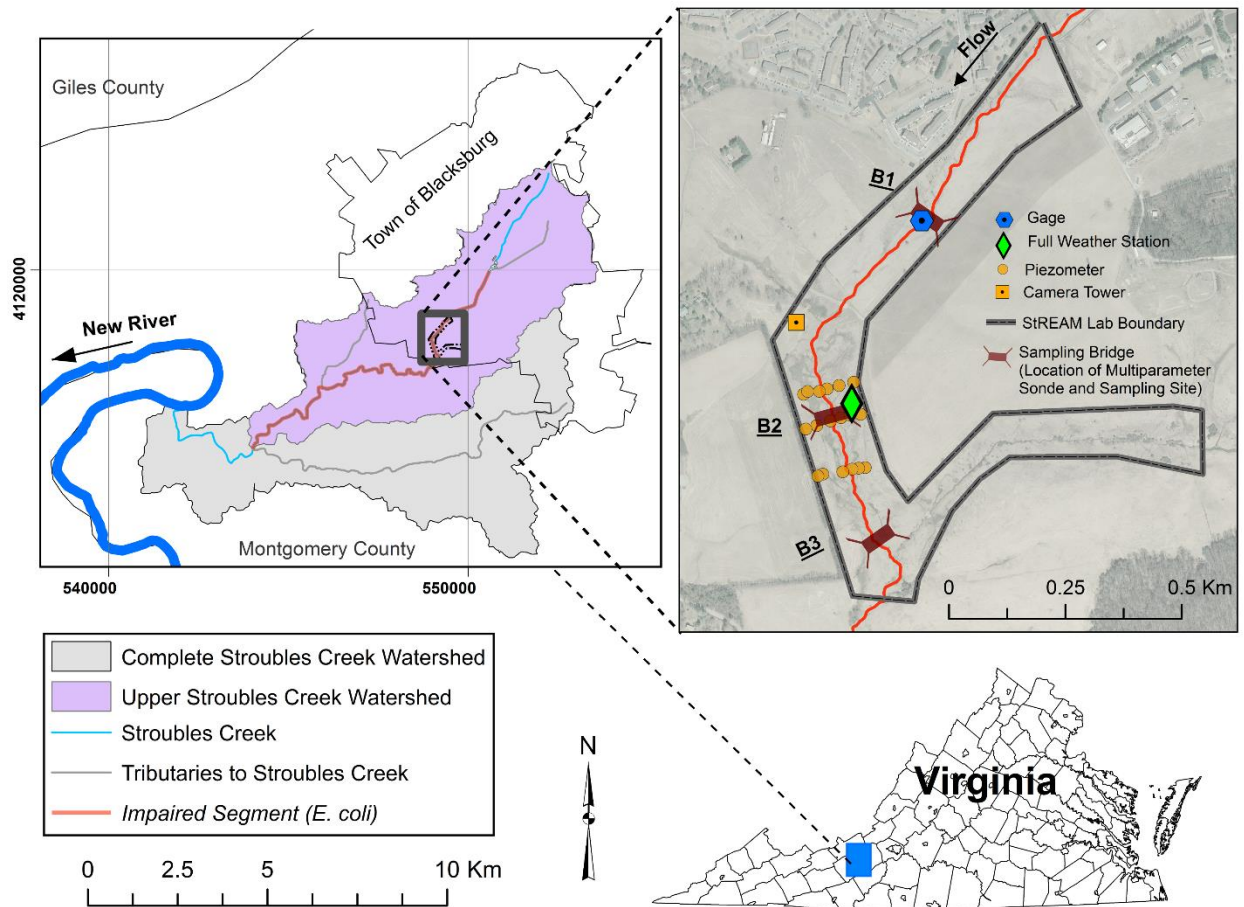


Figure 2-2. Location of Stroubles Creek watershed, StREAM Lab, and monitoring sites (B1: sampling bridge 1; B2: sampling bridge 2; B3: sampling bridge 3).

2.2.2. Sampling design

Water and underlying sediment samples were taken from three sites within the StREAM Lab corresponding to the existing sampling access bridges. In Figure 2-2, from upstream to the downstream, the three sampling sites are designated as B1, B2, and B3. Site B2 is located approximately 550 m downstream of B1, and B3 is approximately 330 m downstream of B2. Both banks are covered with thick grassy vegetation. At baseflow conditions, the water depth of this segment varied from 13 cm to 33.5 cm, and the channel width varied from 2.7 m to 4.0 m (Abel, 2012). Physicochemical water-quality variables (e.g. stream water temperature, specific

conductivity, pH, turbidity, and dissolved oxygen) are continuously monitored by multi-parameter water-quality sondes (YSI Inc., Yellow Springs, OH) at all three sites. Stage is monitored via a gage (Campbell Scientific, Inc., Logan, UT) at B1, which was converted to flow rate using an existing stage-discharge equation developed by the StREAM Lab using the velocity-area method (NRCS, 2014). Hourly rainfall is recorded by a full weather station (Campbell Scientific, Inc., Logan, UT) near B2.

Grab samples of water and sediment from the three sampling bridges were collected weekly for one year (February 2012-January 2013), i.e. a total of 50 samples per sampling site. Samples were collected from the most downstream to most upstream site to avoid contamination via upstream re-suspension. Water samples were collected in sterile 250 mL wide-mouth polypropylene bottles. Although studies have shown that FIB can penetrate the hyporheic zone even in fine-grained bedded streams (Drummond et al., 2014), it is largely assumed that most FIB are retained in the upper layer of bed sediment (i.e. the top few centimeters associated with sedimentation and re-suspension) (Kim et al., 2010). Therefore, in this study, sediment samples were collected from approximately the upper one cm of bed sediment, and triplicate sediment samples from each site were composited in a sterile Whirl-Pak bag as recommended previously by Myers et al. (2007). The time of day was recorded following sampling, and samples were transported to the laboratory on ice within one hour and promptly analyzed.

2.2.3. Laboratory analysis

Two FIB targets, *E. coli* and enterococci, were analyzed in this study. Although only *E. coli* is currently monitored by the VADEQ to ensure standards compliance (SWCB, 2010), both *E. coli* and enterococci are recommended by the 2012 USEPA Recreational Water-Quality Criteria (RWQC) for freshwater monitoring (USEPA, 2012b)..

Water samples

Concentrations of *E. coli* and enterococci were determined via the Colilert and Enterolert defined substrate techniques, respectively (IDEXX Laboratories, Inc., Westbrook, ME, USA). Quantification through incubation in the 97-well Quanti-tray/2000 permitted calculation of most-probable-number (MPN) based concentrations (Hurley and Roscoe, 1983). Colilert trays were incubated at 37°C for 24 h, and Enterolert trays were incubated at 41°C for 24 h per manufacturer recommendations. Following incubation, fluorescent wells within each Quanti-tray/2000 were enumerated under a 6-watt, 365-nm handheld UV lamp Model UVL-56 (UVP LLC, Upland, CA, USA). The bacteria concentrations in water samples were expressed as most-probable-number per 100 mL water (MPN/100 mL).

Bottom sediment samples

Sediment-microbial aggregates were dispersed prior to quantification by vortexing with Tween-85, which disperses sediment-microbial aggregates as effective as sonication without measurable microbial die-off (Krometis et al., 2009b). For each sample, a wet weight of 3.0 g sediment was mixed with 200 mL distilled water. Forty drops of Tween-85 (approximately 400 µL) were added to the solution, followed by 10-s vortex mixing to produce homogeneous slurry. After allowing the

slurry to settle for 30 minutes, the supernatant was analyzed using the same defined substrate techniques (i.e. Colilert, Enterolert) used in the water sample analysis. Potential quantification errors due to particle-bound organisms during Quanti-tray analysis (e.g. multiple cells per well) have been determined to be minor in most scenarios (Fries et al., 2006). In order to determine the dry weight of sediment samples, 3.0-g subsamples for each site were dried at 40°C for 24 h. FIB concentrations in the bed sediments were expressed as most-probable-number per gram dry sediment (MPN/gds).

2.2.4. Hydrometeorological and physicochemical variables

Continuous monitoring records for hourly rainfall, water temperature, stage, specific conductivity, pH, dissolved oxygen, and turbidity were available for the February 2012-January 2013 monitoring period from the StREAM Lab database (<http://www.bse.vt.edu/site/streamlab/>). Flow rate was calculated using an existing stage-discharge equation developed by the StREAM Lab. Cumulative antecedent rainfall (Rain x, where x=12 h, 24 h, 48 h, or 72 h) was calculated through summation of the total rainfall in the time x prior to the sampling event.

2.2.5. Statistical analysis

FIB density values were log₁₀ transformed to reduce skewness, as visually confirmed by a quantile-quantile plot (QQ plot) of the standardized data against the standard normal distribution (for normal data, the points plotted in the QQ plot should fall approximately on a straight line). Spatial variations in FIB concentration between sites were examined via one-way analysis of variance (ANOVA). The Pearson product-moment correlation coefficient (r) was used to test for correlations between FIB in water column and FIB in bed sediment (log₁₀ transformed data were

used). Because the skewness of other physicochemical variables was not reduced sufficiently by log10 transformation for parametric Pearson product-moment correlation analysis, non-parametric Spearman's rank correlation coefficient analysis was employed to test the monotonic relationships with FIB. All statistical analyses in this study were performed in R version 2.15.3 (R Development Core Team, 2013).

2.3. Results and discussion

Differences between observations of FIB concentration were not statistically significant for any of the three sampling bridges (ANOVA test, $p > 0.2$). Therefore, FIB concentrations from the three sites in each sampling event were pooled to compare with the water-quality standards. The geometric mean of the FIB concentrations corresponding to the three sampling bridges in each sampling event were used in the correlation analysis with discharge and rainfall, as there is only one stage recorder at B1 and one full weather station close to B2 (Fig. 2-2). As there are no significant flow inputs between the three sampling bridges, it appears reasonable to assume the flow rates are similar.

2.3.1. Statistics of FIB concentrations in the water column and a comparison with multiple standards

The distribution of FIB concentrations in water samples by month (February 2012 to January 2013) is shown in Figure 2-3. The observed monthly geometric mean of *E. coli* concentrations in the water column ranged from 70 MPN/100 mL (November) to 1000 MPN/100 mL (September), with a median value of 290 MPN/100 mL (Figure 2-3a and Table 2-1). The monthly geometric mean

of enterococci concentrations ranged from 4 MPN/100 mL (Mar) to 290 MPN/100 mL (September), with a median value of 40 MPN/100 mL (Figure 2-3b and Table 2-1).

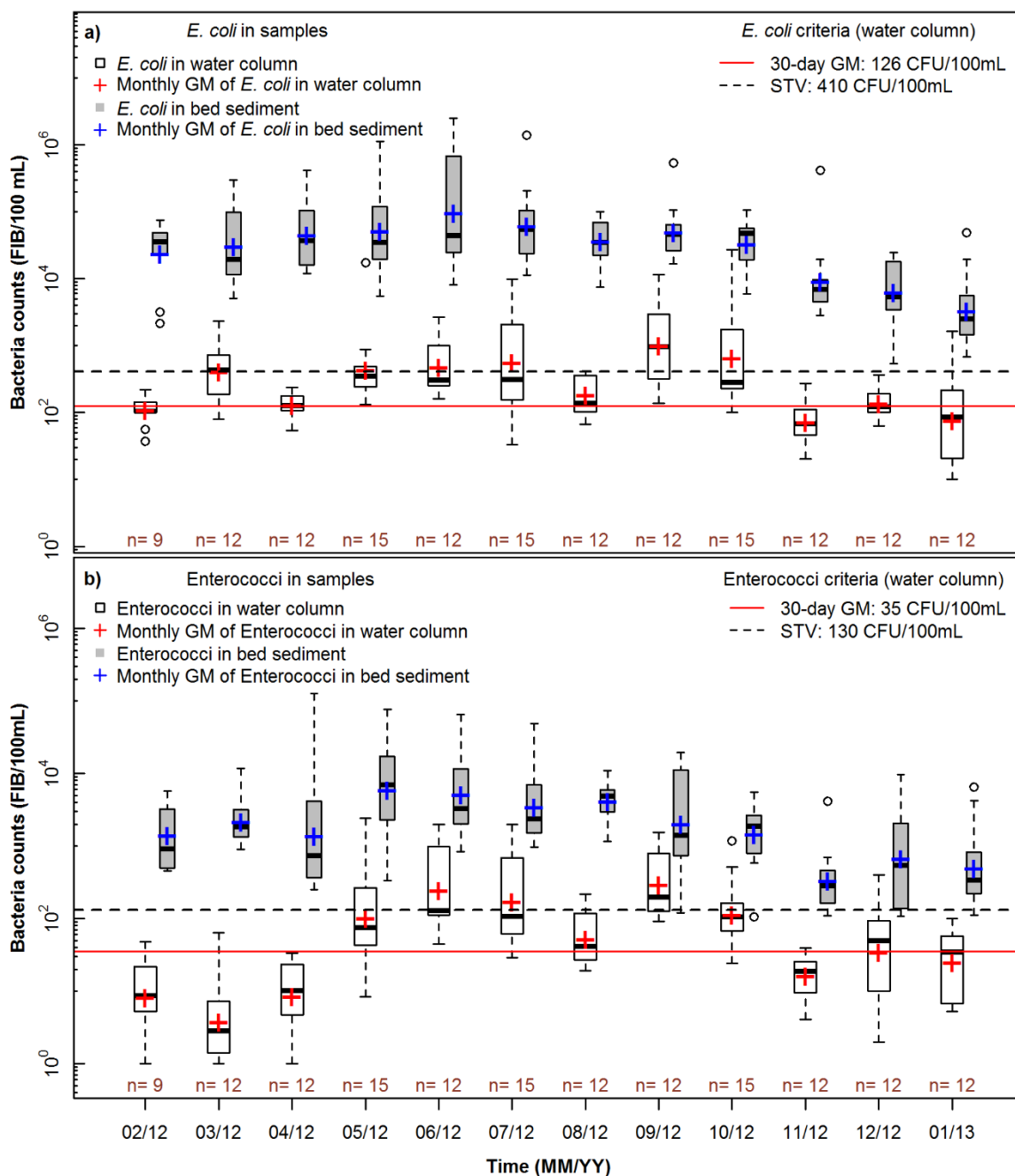


Figure 2-3. Monthly distribution of (a) *E. coli* concentrations in the water column and streambed sediments, and (b) enterococci in the water column and streambed sediments (the upper and lower whiskers represent 90th and 10th percentiles, respectively; the box show

Table 2-1. Summary of statistics of monthly geometric mean of FIB concentrations in the bed sediment, water column, and the ratio.

		Min	Max	Median; Arithmetic Mean
Monthly geometric mean of <i>E. coli</i> concentrations in	Sediment (MPN/100 mL)	3300 (Jan)	95000 (Jun)	34000; 37000
	Water (MPN/100 mL)	70 (Nov)	1000 (Sep)	290; 350
	Sediment / water	40 (Dec)	350 (Apr)	110; 130
Monthly geometric mean of enterococci concentrations in	Sediment (MPN/100 mL)	330 (Nov)	5900 (May)	1700; 2400
	Water (MPN/100 mL)	4 (Mar)	290 (Sep)	40; 90
	Sediment / water	7 (Sep)	580 (Mar)	20; 100

It is worth noting that the decision to include Stroubles Creek on the Virginia 303(d) list of impaired waters was made based on the observation that approximately 8 of 32 samples (25%) collected by the state exceeded the 235 CFU *E. coli* /100mL single sample maximum criterion during any 2-year period from 2006 to 2012 (VADEQ, 2014). In 2012, the USEPA released revised recreational water-quality standards based on the use of two bacterial indicators (*E. coli* and enterococci) and two magnitude measures (Geometric Mean and Statistical Threshold Value) (Table 2-2). Although adherence to the new water-quality guidelines is not required, they are intended as guidance to each state in establishing new standards. Figure 2-3 therefore illustrates a comparison of FIB measurements with both the existing state standard and the 2012 USEPA revised standard. Overall, similar exceedance rates (9 out of 12 months) were observed by using the state standard and the revised USEPA guidelines (Figure 2-3).

Table 2-2. Bacteria criteria to protect waters designated for primary contact recreational uses: Virginia surface water quality criteria as established in Jan 2011, and USEPA 2012 recreational water quality criteria recommendations for protecting human health in all coastal and noncoastal waters. (Standards from Recommendation 1 is plotted to evaluate the Stroubles Creek microbial water quality)

Fecal Indicator Bacteria (FIB)	VA bacteria criteria (CFU/100 mL)		USEPA 2012 recommendations (CFU/100 mL)			
	30-day GM[a]	Single-sample[b]	Recommendation 1[c]		Recommendation 2 [e]	
			30-day GM	STV[d]	30-day GM	STV
<i>E. coli</i> (fresh)	126	235	126	410	100	320
Enterococci (marine & fresh)	35 (transition and saltwater)	104 (transition and saltwater)	35	130	30	110

[a] GM = geometric mean;

[b] No more than 10% of the total samples in the assessment period shall exceed the single-sample criteria;

[c] Recommendation 1 based on an estimated illness rate of 36/1,000;

[d] STV = statistical threshold value. Approximates the 90th percentile of the water quality distribution and is intended to be a value that should not be exceeded by more than 10% of the samples taken;

[e] Recommendation 2 based on an estimated illness rate of 32/1,000.

2.3.2. Statistics of FIB concentrations in the streambed sediments and a comparison with overlying water FIB concentrations

FIB concentrations in the streambed sediments were compared with FIB concentrations in the water column. The sediment FIB concentrations were converted from MPN/gds (gds=grams of dry sediment) to MPN/100 mL by sediment density as described previously (Buckley et al., 1998). The monthly geometric mean of *E. coli* concentrations in the sediment during the period of study ranged from 3300 MPN/100 mL (January) to 95000 MPN/100 mL (June), with a median value of 34000 MPN/100 mL (Figure 2-3a and Table 2-1). The monthly geometric mean of enterococci concentrations in the sediment ranged from 330 MPN/100 mL (November) to 5900 MPN/100 mL (May), with a median value of 1700 MPN/100 mL (Figure 2-3b and Table 2-1).

Ratios of the monthly geometric mean of *E. coli* concentrations in the bed sediments to that in the water column ranged from 40 to 350 (Table 2-1), while the ratio of the monthly geometric mean of enterococci concentrations in the bed sediments to that in the water column ranged from 7 to 580 (Table 2-1). While the present study represents an initial attempt to include sediment samples in a regular FIB monitoring effort for an inland urban stream, these results agree with previous studies of streambed sediment grab samples that observed higher FIB concentrations per unit volume as compared to overlying water column concentrations. Buckley et al. (1998) observed that total coliform concentrations in bottom sediments were on average 1000 times higher than in the overlying water column in a subtropical rainforest conservation reserve, where sediment samples were taken on twelve occasions during November 1993 to April 1994. An et al. (2002) reported that *E. coli* concentrations in sediments were more than 10000 times higher than in the water column based on a two-day observation in an inland lake, and Pandey et al. (2011) documented that concentrations of *E. coli* in streambed sediments were 2 to 90 times higher than concentrations in the water column during a one-day observation of different locations along an agricultural creek in summer. Comparisons between these limited references may suggest that ratios of FIB concentrations in bottom sediments to that in the water column in urban streams are lower than lakes or reservoirs, but are higher than agricultural streams. It is worth noting that the transport of sediment-associated FIB in urban streams can have more severe impacts on downstream water-quality as compared to agricultural streams due to the intense hydrologic alterations in urban areas, which results in both increased frequency and magnitude of high-flow events (Wenger et al., 2009).

2.3.3. Correlations with hydrometeorological and physicochemical factors

A summary of available hydrometeorological and physicochemical variables corresponding to the sampling time over the study period, their sources, and statistics is provided in Table 2-3. The Spearman rank correlation coefficient (ρ) was used to identify key hydrometeorological and physicochemical water-quality variables that correlated with water and sediment FIB concentrations (Table 2-4). Statistical significant correlation coefficients ($\alpha=0.05$) are discussed below.

Table 2-3. A summary of data statistics and their sources (data corresponded to the sampling time)

Variables	Sources	Monitoring frequency	Maximum observation	Minimum observation	Median observation	Arithmetic Mean
Hourly Rainfall (mm)	StREAMLab	1 hour	0.51	0	0	0.02
Antecedent 12 h Rainfall (mm)	Aggregated		34	0	0	2
24 h			34	0	0	4
48 h			34	0	2	6
72 h			349	0	6	15
Water temperature (°C)	StREAMLab	15 min	25.5	-0.1	14.9	13.6
Dissolved oxygen (mg/L)	StREAMLab	15 min	15.5	6.3	9.8	10.1
Specific conductivity (mS/cm)	StREAMLab	15 min	0.86	0.001	0.49	0.40
Flow (cms)	StREAMLab	10 min	0.26	0.03	0.08	0.09
Turbidity (NTU)	StREAMLab	15 min	992	0.2	5.3	25.4
pH	StREAMLab	15 min	8.1	5.9	7.7	7.7

2.3.3.1. FIB concentrations in the water column

Overall, both increases in *E. coli* and enterococci concentrations in the water column were strongly correlated with increases in antecedent 24-h rainfall, increases in stream water temperature, and decreases in dissolved oxygen (Table 2-4, Spearman's correlation coefficient $\rho \geq 0.35$). While several previous studies have also observed positive correlations of water FIB concentrations with 24-h antecedent rainfall (Mallin et al., 2001) and stream water temperature (He et al., 2007), these relationships do not appear consistent. Gentry et al. (2006) observed negative correlations between stream water temperature and water FIB concentrations in a southeastern stream within a mixed

land use watershed with karstic features, whereas Vidon et al. (2008) found no correlation between stream water temperature and water FIB concentrations in midwestern streams, and Kelsey et al. (2004) found antecedent 48-h rainfall correlated better with water FIB concentrations than antecedent 24-h rainfall in a high-salinity estuary draining a urbanized watershed in South Carolina coast. Therefore, consistent correlations between these variables and water FIB concentrations are not well-established, which is probably due to temporal and spatial complexity of different watersheds. It is likely necessary to establish correlations between water FIB concentrations and environmental variables for a specific site or a watershed type to facilitate long-term predictive modeling purposes.

Table 2-4. Summary of Spearman's rank correlation ρ ($\alpha = 0.05$).

	FIB concentrations in water (MPN/100mL)		FIB concentration in sediment (MPN/gds)	
	waterEC	waterENT	sedEC	sedENT
Hourly rainfall (mm)	-	-	-0.33	-0.29
Antecedent rainfall (mm)	12 h	0.34	-	-
	24 h	0.40	0.28	0.30
	48 h	0.33	-	0.39
	72 h	-	0.30	0.52
Stream Temperature (°C)	0.47	0.53	0.48	0.50
Dissolved oxygen (mg/L)	-0.51	-0.73	-0.35	-0.36
Specific conductivity (mS/cm)	-	-0.43	-0.26	-0.24
Stage (m)	0.38	-	-	-
Turbidity (NTU)	0.19	-	-	-
pH	-	-0.31	-	-

(Normal font: $p < 0.05$; ‘-’: $p > 0.05$)

2.3.3.2. FIB concentrations in the streambed sediments

As FIB concentrations in the streambed sediments are not currently monitored or regulated by environmental agencies, long-term monitoring data of sediment FIB concentrations are rare. Comparison of these observations with correlations observed for water FIB concentrations does provides insight into key hydrometeorological and physicochemical variables, which should be the focus of later model refinements or remediation efforts.

Hydrometeorological variables

Increases in hourly rainfall (i.e. the total rainfall in the one hour preceding a sampling event), though not correlated with overlying water FIB concentrations, were significantly correlated with decreases in sediment FIB concentrations ($p < 0.05$). Increases in antecedent 24-h rainfall were significantly correlated with increases in both water and sediment FIB concentrations ($p < 0.05$). This may suggest antecedent accumulative 24-h rainfall is generally a good indicator of FIB wash-off from upland watershed surfaces and sedimentation.

Increases in stream flow, though correlated with increases in water *E. coli* concentrations ($p < 0.05$), were not correlated with sediment FIB concentrations in this study ($p > 0.05$). Although previous studies have indicated that FIB loadings to receiving waters were dominated by hydrological events (Muirhead et al., 2004; Davies-Colley et al., 2008; Wilkinson et al., 2011), it is important to note that in this study samples were mostly taken during dry-weather (i.e. low flow) conditions. The absence of correlation between flow and sediment FIB concentrations might therefore be a result of relatively stable flow conditions. Examining how sediment FIB respond to a wider range of flow conditions is an important need for future model development.

Physicochemical variables

Stream water temperature was positively correlated with FIB concentrations in both the water column and bottom sediments ($p < 0.05$). Water temperature has long been recognized as a critical environmental factor in the survival of FIB (Ferguson et al., 2003; Hipsey et al., 2008; Bradford et al., 2013b). Under laboratory conditions with other variables (i.e. pH, salinity) held constant at ideal conditions, coliform bacterial survival was inversely proportional to water temperature, i.e.

cells remained culturable longer at lower temperatures (McFeters and Stuart, 1972). In the natural environment, however, water temperature can be a surrogate for multiple environmental and landuse factors that impact FIB inputs and survival. While higher water temperatures may be more likely to increase bacterial inactivation/die-off rates, they also generally signal greater potential for fecal inputs (e.g. more livestock, greater wildlife and pet activity) and regrowth. There is no consensus from previous studies regarding temperature impacts; negative (Gentry et al., 2006), positive (He et al., 2007), and no (Vidon et al., 2008) correlation between water temperature and water FIB concentrations have been observed. In the Virginia Ridge and Valley region, more frequent storm events during the warmer seasons results in greater fecal, nutrient, and sediment loadings to the stream, which may create a more favorable environment for bacteria survival and potential growth in both the water column and bed sediments. It is also possible that more fecal inputs into the stream during warmer months simply offset the rapid inactivation/die-off rates at higher water temperatures.

Increases in specific conductivity and dissolved oxygen were significantly correlated with decreases in FIB concentrations in bed sediments, in a manner similar to that of water enterococci concentrations. Previous studies have observed decreased water FIB concentrations in laboratory conditions when specific conductivity raised from 1.2 to 6.7 mS/cm (Singleton et al., 1982), in natural ponds when specific conductivity rose above 5 mS/cm (He et al., 2007) and in streams when specific conductivity increased (value unreported) (Gentry et al., 2006), suggesting high salt concentrations accompanied with high levels of specific conductivity can inhibit microbial growth or even damage cells (Singleton et al., 1982; Gentry et al., 2006; He et al., 2007; Bradford et al., 2013b). In this study, no correlation was observed between specific conductivity and *E. coli*

concentration in the water column, which is not surprising as a previous study has reported minimal photo-oxidative damage to *E. coli* at low salinity conditions (the specific conductivity levels observed at this site ranged from 0.001 to 0.86 mS/cm, table 3-2) (Sinton et al., 2002). Negative correlations between sediment FIB concentrations and specific conductivity were unexpected, as specific conductivity has been previously identified as a factor encouraging microbial-sediment attachment (Bradford et al., 2013b). It is very possible that other factors dwarfed this effect, i.e. increases in specific conductivity have found to be concurrent with rainfall events in this site (data not shown), which may disturb streambed sediments and release attached FIB.

The negative correlations between FIB concentrations and dissolved oxygen levels may be the result of increased waste inputs to the stream, which would be expected to simultaneously increase bacteria growth and biological oxygen demand (BOD). In addition, increases in dissolved oxygen levels can result from lowered water temperature due to substantial underground water recharge at this site, which may also dilute the FIB concentrations. It is also possible that sunlight-induced inactivation (i.e. photo-oxidative effects) of FIB in the water column increased with sufficient dissolved oxygen in the stream (Sinton et al., 2002; Hipsey et al., 2008), which may also affect the FIB in the bed sediment given high clarity of the creek when the level of dissolved oxygen is high and the creek is shallow (i.e. less than 0.23 meter) at dry-weather conditions.

No significant correlations were found between sediment FIB concentrations and pH over the course of this study. This may be due to relatively stable pH values (range: 5.6-8.1) within Stroubles Creek (Table 2-3), and previous studies suggested minimal effect of pH on bacteria survival at levels between 6 and 8 (Foppen and Schijven, 2006; Hipsey et al., 2008; Bradford et

al., 2013b). Correlations between turbidity and sediment FIB concentrations were also not significant in this study. Although turbidity is sometimes regarded as a general measure of nonpoint source contamination to urban streams, observations of relationships between FIB and turbidity levels in previous studies have been mixed. While several studies found positive correlations between turbidity and water FIB concentrations at near low flow conditions (Mallin et al., 2001; Reeves et al., 2004; He et al., 2007) and over hydrograph events (Davies-Colley et al., 2008), other studies observed no significant correlation (Gentry et al., 2006; He et al., 2007; Vidon et al., 2008). These observations suggest that caution is needed before uncritically using turbidity as an indicator of FIB contamination.

2.4. Conclusions

Observations of streambed sediments harboring 40 to 350 times the *E. coli* concentrations of the overlying water column, and 7 to 580 times the enterococci concentrations of the overlying water column are in agreement with many previous studies highlighting the potential for FIB sediment storage. Ratios in this study were generally higher than those previously reported for an agricultural stream, which may suggest the importance of considering watershed-specific landuse when modeling FIB behavior.

Key hydrometeorological and physicochemical variables influencing both water and sediment FIB concentrations were identified in this study, including antecedent accumulative 24-h rainfall and water temperature. Increases in antecedent accumulative 1-h rainfall were associated with decreases in sediment FIB concentrations, supporting previously presented studies suggesting initial storm surges “flush” (re-suspend) sediment bacterial reservoirs (Jamieson et al., 2005b;

Pandey et al., 2011; Ghimire and Deng, 2013); though higher sediment FIB concentrations were associated with greater antecedent 24-hour rainfall amounts, suggesting that over time these sediments may be “re-seeded” by further FIB loadings, as suggested previously (Russo et al., 2011). However, it is important to recognize that while these results might support the previous findings of other researchers as discussed, because these samples were taken weekly rather than throughout a single storm, they cannot confirm this behavior to be the cause of the observed fluctuations in FIB concentrations. Future intra-storm studies would be essential to quantitatively estimate the degree to which re-suspended sediment FIB contributes to downstream concentrations. It appears understanding the relative importance of these two competing factors (sediment “flush” vs sediment “seeding”) would greatly improve the understanding of FIB transport that underlies model development.

Comparison of observations in this study to previously reported studies indicated that factors commonly associated with general non-point source pollution (e.g. turbidity, flow) may not be universally associated with FIB levels in all watershed types. This may be the result of differences in water chemistry (fresh vs. salt water), geographical region (patterns of baseflow and storm magnitude), and/or upland landuse. Further refinement of models should consider whether or not the sediment-related transport processes in FIB simulations are broadly applicable beyond the watershed-specific datasets used in model development.

Acknowledgments

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Chapter 3. Storm loads of culturable and molecular fecal indicators in an inland urban stream

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Abstract

Elevated loading of fecal contamination in receiving waters during wet-weather flows is a considerable public health concern that can be exacerbated by climate change and urbanization. However, current understanding of the fate and transport of fecal indicator bacteria in stormwater is limited, and even less is known about molecular fecal indicators, which may supplant traditional culturable indicators. In this study, concentrations and loading rates of both culturable and molecular fecal indicators were quantified at high temporal frequencies in an instrumented inland urban stream during six storm events. While both concentrations and loading rates of each fecal indicator increased rapidly during the rising limb of the storm discharge hydrographs, it is the loading rates rather than instantaneous concentrations that provides a better estimate of transport through the stream during the entire storm. Overall, indicator source, rather than type, played the most important role as general fecal indicators (both culturable and molecular) correlated most highly with each other during storm events but not with a human associated marker. Event loads of general fecal indicators were most strongly correlated with total runoff volume, maximum discharge and maximum turbidity. Event loads of human-associated *Bacteroides* were most strongly correlated with the time to peak flow in a hydrograph. Sampling multiple points spanning the whole hydrograph with higher frequency during the rising limb is critical to improve estimates of pollutant load.

3.1. Introduction

Fecal pollution from agricultural operations, human-derived sources, domestic animals and wildlife can be disproportionately transferred to receiving waters during intermittent storm events, potentially leading to the downstream dissemination of pathogens (Ford and Colwell, 1996;

Krometis et al., 2007; Collier et al., 2012). This represents a considerable public health concern and challenge in watershed management. An increase in the frequency and magnitude of storm events is predicted given anticipated climate change, with the most dramatic effects expected in urban areas due to their altered landscapes and hydrology. Consequently, efforts to better understand sources, transport processes, and accompanying risks associated with fecal indicator bacteria (FIB) in urban stormwater runoff continue to receive substantial attention (Gaffield et al., 2003).

The majority of previous studies have relied upon the collection and analysis of single grab samples of surface waters during high-flow events to understand relationships with major environmental factors such as land use and hydro-meteorological variables (Mallin et al., 2001; Kelsey et al., 2004; Reeves et al., 2004; Gentry et al., 2007; Vidon et al., 2008; Liao et al., 2014). However, samples collected at single time points do not account for concentration changes during the course of a storm and therefore provide limited information regarding how loading rates might fluctuate during storm events. Pollutant loading information is critically important for watershed managers, as the current regulatory strategy informing remediation efforts is the Total Maximum Daily Load (TMDL) program under the U.S. Clean Water Act's sections 305(b) and 303(d), which quantifies target reductions in contamination per source in terms of loads rather than concentrations (Benham et al., 2011). Recent studies that have analyzed multiple discrete samples per storm event have noted that a single storm in an urban watershed could transport the same FIB loads as multiple years' of dry-weather loads, further emphasizing the need to focus on reduction in stormwater levels of fecal contamination to reduce downstream impacts and exposure risks (Krometis et al., 2007).

Previous estimates of stormwater microbial loads have focused exclusively on levels of culturable FIB (e.g., *E. coli*, enterococci) (Surbeck et al., 2006; Hathaway et al., 2010; McCarthy et al., 2013), so little is known regarding the transport of emerging microbial source tracking (MST) indicators. Focusing on the transport of culturable FIB remains important given current regulatory standards and programs that list maximum permissible culturable FIB concentrations in terms of coliform-forming-unit (CFU) per 100 mL. However, it appears likely that qPCR methods will eventually supplant culture-based methods as the monitoring mechanism of choice. Compared to culture-based methods, qPCR methods are advantageous in situations that require quick regulatory decision (e.g., beach closures) (Griffith et al., 2009), and situations that need to quantify relative contributions of different pollutant sources in order to aid in prioritizing remediation efforts (Sauer et al., 2011). Given that MST markers generally target genetic material via quantitative polymerase chain reaction (qPCR), rather than viable organisms, their transport dynamics during stormflows may be different. This represents an important knowledge gap in developing improved approaches to watershed management and research is needed to investigate the relationships between the two method endpoints and understand associations with environmental variables.

The goal of this study was to quantify the transport of culturable and molecular fecal indicators in an inland urban stream during storm events. The specific objectives were to: 1) contrast the intra-storm patterns of concentrations and loading rates of culturable and molecular fecal indicators throughout each storm; 2) estimate the total event load of each fecal indicator during each storm; and 3) investigate how storm-induced event loads of different fecal indicators relate to a variety of hydro-meteorological and physicochemical factors. High-frequency samples were collected

during six summer storms in 2013, and analyzed using multiple methods to generate concentrations of culturable *E. coli* (EC), culturable enterococci (ENT), *Enterococcus* spp. 23S rRNA gene copies (ENT-23S) (Haugland et al., 2005), and the human-associated HF183 *Bacteroides* 16S rRNA gene copies (HF183) (Seurinck et al., 2005) for each sample. As the focus of this present study is to explore the similarities and differences of culturable and molecular fecal indicators rather than develop or improve detection methods, the four relatively well-developed detection methods were selected, and protocols from previous literature were followed.

3.2. Materials and methods

3.2.1. Study area description

Samples were collected at a sampling bridge at Virginia Tech Stream Research, Education, and Management Laboratory (StREAM Lab) along Stroubles Creek in Blacksburg, VA, USA (Thompson et al., 2012). The 15-km creek, classified as a recreational water, runs from northeastern Blacksburg, through the Virginia Tech campus, and then into the New River, which has been the region's main source of drinking water supply and home to various recreational activities since the 1950s. A segment of the creek is instrumented with real-time monitoring capacity for a variety of hydro-meteorological and physicochemical variables as described in previous studies (Thompson et al., 2012; Liao et al., 2014). The watershed that drains to the sampling site encompasses an area of 14.4 km² that classified as 84% urban/residential, 13% agricultural, and 3% forested (Fig. 3-1). The average annual precipitation is 103.9 cm (40.9 in) with 30% of this precipitation occurring during the summer (June-August). The average temperature in summer is 20.9 °C (69.7 °F), with a minimum of 14.7 °C (58.4 °F) and a maximum of 27.2 °C (80.9 °F).

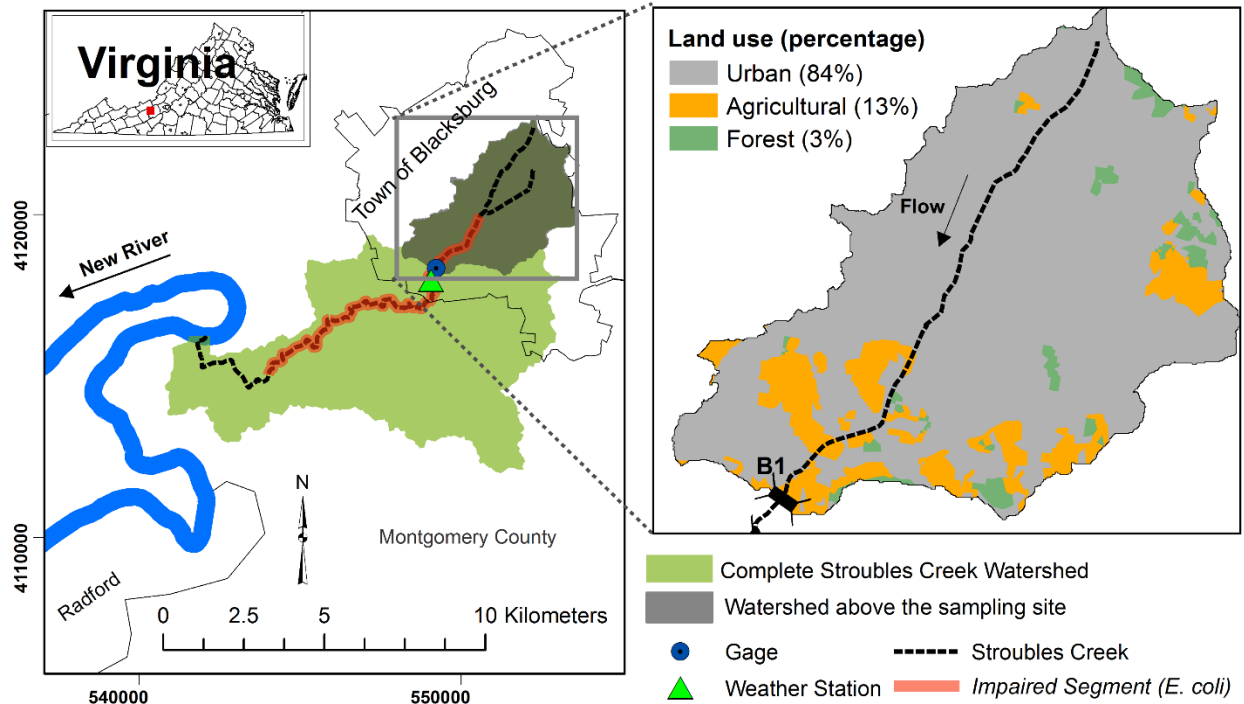


Figure 3-1. Location and land use distribution of upstream watershed above the sampling bridge – B1 (Map projection: NAD83 / UTM zone 17N; land cover data source: NLCD 2006 <http://nationalmap.gov/>).

Growth and urbanization is rapidly changing the Stroubles Creek watershed and stream hydrology (VADEQ and VADCR, 2006). Accordingly, the Town of Blacksburg has recently been classified as a small urban center under the MS4 program. Storm and sanitary sewers are entirely separate. A Total Maximum Daily Load (TMDL) implementation plan was established in 2006 to address violation of the general biological integrity clause of the Clean Water Act; reduced benthic macro-invertebrate abundance and diversity was assumed to be mainly the result of excessive sediment loads.(VADEQ and VADCR, 2003; VADEQ and VADCR, 2006) In 2008, the 11.6-km segment of the creek (Fig. 3-1) was added to the state's 303(d) impaired waters list due to elevated *E. coli* levels, with a TMDL specifying reductions in reducing bacteria loads impending (VADEQ, 2010).

3.2.2. Sampling strategy

Discrete water samples were collected automatically via a Teledyne 6712 ISCO sampler (Isco, Inc., Lincoln, NE, USA) during six summer storms (June 26, June 27, June 30, July 2, July 10, and July 21, 2013). Prior to an anticipated storm event, the ISCO was loaded with 24 pre-sterilized sampling bottles and programmed for equal-volume (i.e. 750 mL) sampling at constant intervals (i.e. 15 min or 30 min). The ISCO was triggered manually based on the immediate observations of actual rainfall within the watershed. Samples were kept on ice and retained for analysis if discharge and turbidity values (continuously monitored in real-time at the StREAM Lab) were higher than the observed average dry-weather values. In addition, three grab samples were collected during dry-weather conditions, defined as no rainfall for the previous 24 hours (June 25, July 9, and July 16, 2013). These samples provided baseline FIB concentrations to enable comparison with wet-weather FIB concentrations. All samples were preserved on ice during transport and stored at 4°C for less than 24 hours in the Water Microbiology Lab of Virginia Tech prior to analysis.

3.2.3. Laboratory analyses

Concentrations of culturable *E. coli* and enterococci in each sample were measured utilizing the Defined Substrate Technology® kits, Colilert® and Enterolert® (IDEXX Laboratories, Inc., Westbrook, ME, USA), respectively. All samples were diluted with reagent-grade water by 1:100 prior to analysis following the manufacturer's instructions. Both tests used the Quanti-Tray®/2000 for enumeration of cells, and the number of positive wells were converted to Most Probable Number (MPN) per 100 mL water via the MPN generator software (IDEXX, 2015), additional 50 mL from each sample was filtered through a Millipore™ Isopore™ Polycarbonate Membrane Filter (0.4 µm pore size, 47mm diameter; Fisher Scientific, Pittsburgh, PA, USA) and stored in 2-

mL sterile cryotubes at -80°C for future qPCR analyses. DNA was extracted from the filters via the PowerSoil® DNA Isolation Kit (MO BIO Laboratories, Inc., Carlsbad, CA, USA) according to the manufacturer's protocol. Filters were cut into smaller fragments with sterile razor blades prior to addition to the PowerBead Tubes to maximize DNA removal. Extracted DNA concentrations were quantified using the Qubit® dsDNA BR Assay kit (Life Technologies, Grand Island, NY, USA), following the manufacturer's instructions.

qPCR assays were performed using previously published methods for the *Enterococcus* spp. 23S rRNA genetic marker (Haugland et al., 2005), and the human-associated HF183 *Bacteroides* 16S rRNA genetic marker (Seurinck et al., 2005). In brief, qPCR reaction mixtures to detect ENT-23S consisted of 12.5 µl of 2×iTaq™ universal probes supermix (BioRad, Hercules, CA, USA), 500 nM each primer, 400 nM probe, 2 mg/mL bovine serum albumin (Fisher Scientific, Pittsburgh, PA, USA), and 5 µl DNA template (sample DNA extracts containing 15ng total DNA, or 10 to 10⁷ copies of plasmid standards). The total reaction volume was adjusted to 25 µl with PCR-grade water (MO BIO Laboratories, Inc., Carlsbad, CA, USA). The reaction mixtures for HF183 contained 12.5 µl of 2×iTaq™ universal SYBR Green supermix (BioRad, Hercules, CA, USA), 300 nM each primer, and 5 µl DNA template (sample DNA extracts containing 15ng total DNA, or 10 to 10⁷ copies of plasmid standards), in a total reaction volume of 25 µl adjusted by PCR-grade water. All qPCR reactions were performed in triplicate in 96-well plates using an Eppendorf Mastercycler® ep realplex instrument (Eppendorf North America, Hauppauge, NY, USA). A no-template control (i.e. replacing DNA template with PCR-grade water) was included in each 96-well plate run. The amplification efficiency (E) was estimated from the slope of the log standard curve as $E = 10^{-1/\text{slope}} - 1$. For each 96-well plate run, an efficiency within 0.9 to 1.1 and correlation

coefficient value above 0.99 was considered acceptable. Concentrations of molecular markers were reported as copy number (CN) per 100 mL as described previously (Yun et al., 2006).

3.2.4. Data analysis and statistics

Colilert and Enterolert samples above the maximum detection limit were assigned the highest value within the limits of detection (241,960 MPN/100 mL) and samples below the detection limit were assigned the lowest value within the limits of detection (100 MPN/100 mL), as in similar studies (Converse et al., 2011). Only 4 out of 130 total samples (3%) measured via the Colilert and Enterolert techniques fell into either of these categories. All qPCR results were within the limits of detection (i.e. 10 to 10^7 per 15 ng DNA).

For each monitored storm event, two key parameters were calculated using previously published methods: 1) Event Load (EL), which is the total pollutant load during a storm event (Eq. 3-1) (Chong et al., 2011b; McCarthy et al., 2012; McCarthy et al., 2013); and 2) Equivalent Background Period (EBP), which is the ratio of a storm event load to a dry-weather load during an equivalent time period (Eq. 3-2) (Krometis et al., 2007). Because the continuously monitored 15-min streamflow do not always strictly overlap with the sampling time, the instantaneous loading rates were calculated by multiplying the fecal indicator concentration with the streamflow recorded (or linearly interpolated) at the time of sample collection. The maximum capacity of 24 sampling bottles of the ISCO sampler allowed us to obtain samples from the majority of a storm hydrograph (i.e. rising limb, peak, and partial falling limb of a storm), but not the entire recession to baseline. Therefore, in order to estimate the event load during a storm, the average FIB concentrations

measured during three dry-weather conditions were used as the FIB concentration corresponding to the end of each storm event in keeping with previous studies (Krometis et al., 2007).

$$EL = 10^4 \sum_{i=1}^N Q_i C_i \Delta t \quad (3-1)$$

$$EBP = EL/DL \quad (3-2)$$

Where, $C_i = i^{\text{th}}$ discrete fecal indicator concentration (MPN/100mL); $Q_i = i^{\text{th}}$ discrete discharge (m^3/s); N = total number of discrete concentrations measured; Δt = sampling frequency (s); DL = mean total dry-weather loads in the same duration of the storm event (MPN)

Principal component analysis (PCA) is one of the most popular approaches to reveal relevant information from environmental data by reducing a complex dataset to a lower, and more easily visualized, number of dimensions (Vialle et al., 2011). In this study, by resolving multiple variables into lower dimensional principle components, PCA was used to: 1) identify relationships between measurements of concentrations of culturable *E. coli*, culturable enterococci, the *Enterococcus spp.* 23S rRNA genetic marker, and the human-associated HF183 *Bacteroides* 16S rRNA genetic marker; and 2) investigate the relationships between the event loads of each fecal indicator and various environmental variables that were selected based on availability from our ongoing in-stream monitoring efforts at the StREAM Lab and an extensive literature review of previous studies (Table S1) (McCarthy et al., 2013). During the PCA analysis, in order to eliminate the effect of different units associated with different variables, all variables were standardized to have zero means and unit variance, and eigenvalues and eigenvectors were calculated using the Spearman's rank correlation matrix. All statistical analyses in this study were performed in R version 3.1.1 (R Development Core Team, 2013).

3.3. Results and discussion

3.3.1. Summary of storm events and statistics of FIB concentrations for each storm

The six storm events varied considerably in terms of duration, rainfall depth, and total runoff volume (**Error! Reference source not found.**), reflecting a wide spectrum of wet-weather flow conditions. Single sample measures of fecal indicator concentrations during storms were uniformly high. Concentrations of culturable *E. coli* and enterococci were 5 to 50 times higher than the current Virginia surface water-quality standards (SWCB, 2010). Concentrations of the *Enterococcus spp.* 23S rRNA genetic marker were 10 to 100 times higher than corresponding culturable enterococci concentrations (Fig. 3-2).

Table 3-1. Characteristics of storm events.

StormID (sample size)	S-1 (n=23)	S-2 (n=18)	S-3 (n=24)	S-4 (n=24)	S-5 (n=19)	S-6 (n=22)
Sampling Date	June 26	June 27	June 30	July 2	July 10	July 21
Sampling frequency (min)	15	15	15	30	30	15
Event rainfall depth (mm)	16	6	17	17	12	7
Event duration (hr)	12	7	13	19	23	6
Time to peak flow (hr)	3	1	3	11	3	1
Event runoff volume (m3)	58000	8100	57000	37000	70000	12000

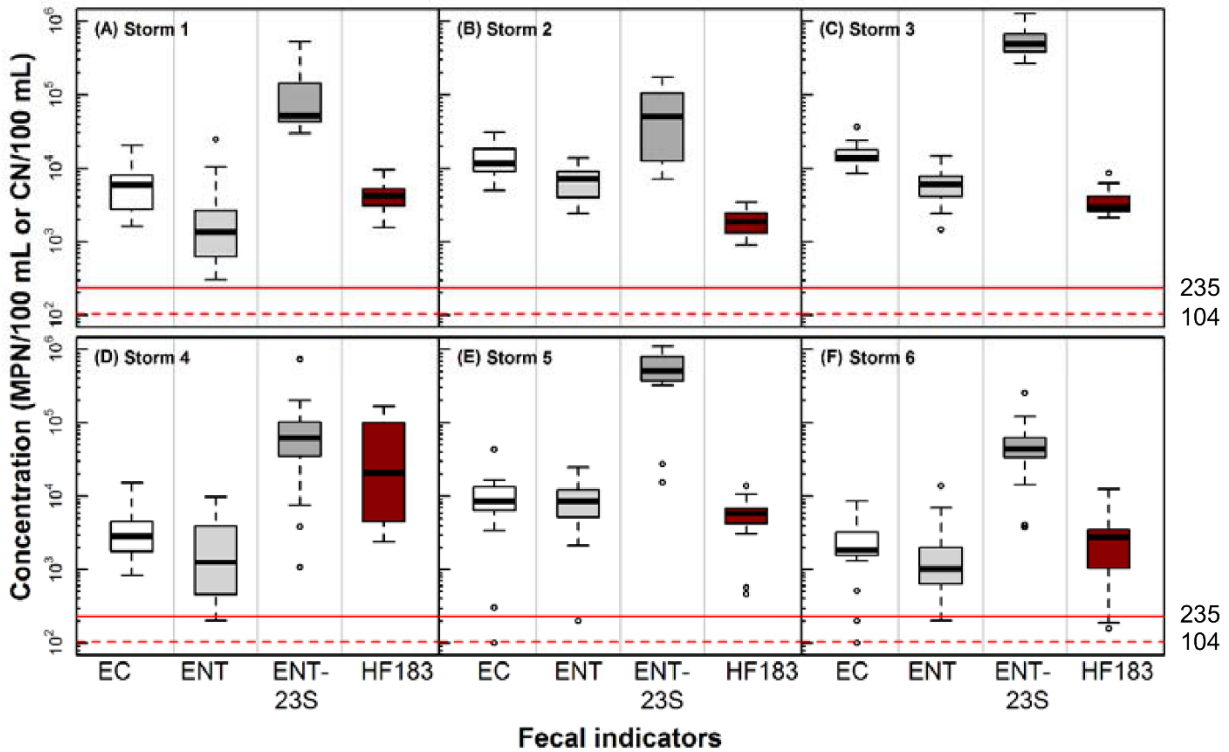


Figure 3-2. Box-and-whisker plot of fecal indicator concentrations over an entire storm. The upper and lower whiskers represent 90th, and 10th percentile, respectively; the box shows 75th, 50th, and 25th percentile; circles represent outliers. The solid red line represents the Virginia recreational water single sample standard for *E. coli* (235 MPN/100mL) and the dotted red line represents a single sample enterococci standard (104 MPN/100mL).

The human-associated HF183 marker was detected in all samples, with median concentrations for each storm ranging from 1000 to 30000 CN/100 mL (Fig. 3-2). There is no regulatory standard for HF183, but these values would be classified as moderate (1000 – 5000 CN/100 mL) to high (>5000 CN/100 mL) according to a recent study of leaking sewer infrastructure in coastal urban areas (Sauer et al., 2011). The HF183 marker was chosen based on the results of a recent multi-laboratory study of the performance of many of the MST markers proposed for water-quality management, which suggested the HF183 marker is one of the most sensitive and specific genetic markers of human fecal contamination (Boehm et al., 2013; Harwood et al., 2013). Although a few

studies have recorded cross-reactivity of HF183 marker with fecal samples from animals (i.e. dog, chicken, duck and deer) (Staley et al., 2012), given that source-tracking was not the primary goal of this study, the potential for cross-reactivity in this watershed was not determined. However, the consistently high levels of HF183 marker in the stream is surprising in a watershed with wholly separate storm and sanitary sewers and several recent source-tracking studies in urban areas suggest that sewage intrusion into storm sewers and urban streams due to aging infrastructure is generally ubiquitous (Marsalek and Rochfort, 2004; Sauer et al., 2011; Guérineau et al., 2014). For the purposes of TMDL implementation, more rigorous source tracking research is needed to confirm the presence of human fecal contamination and identify possible sites of sewage intrusion into the storm sewer system.

3.3.2. Intra-storm patterns of concentrations and loading rates

Concentrations of traditional fecal indicators (i.e., culturable *E. coli* and enterococci) increased rapidly at the beginning of all storms, peaking earlier than the hydrograph, but did not typically decrease as rapidly as stream discharge during the falling limb (Fig. 3-3). Meanwhile, the loading rates of culturable *E. coli* and enterococci generally followed the patterns of the hydrograph more closely, with a rapid increase followed by a more pronounced decrease as stream discharge declined (Fig. 3-4). The intra-storm patterns of *Enterococcus spp.* 23S rRNA marker were quite similar to culturable enterococci in terms of both concentrations and loading rates (Fig. 3-4). This agrees with previous studies that have observed strong correlation between culturable and molecular indicators of *Enterococcus spp.* concentrations at both coastal (Converse et al., 2011) and inland urban watersheds (Krometis et al., 2007; Chong et al., 2011a). While estimates of actual concentrations using the two methods can be quite different as qPCR detects nonculturable and

nonviable cells in addition to live culturable organisms, overall differences in the intra-storm patterns introduced by different methodology were generally quite small (spearman's rank $r = 0.53$, $p < 0.001$). The intra-storm patterns of the human-associated HF183 *Bacteroides* 16S rRNA marker were also quite similar to the other general fecal indicators for most of the storms, except for storm 4, which exhibited decreased concentrations and loading rates at the end of the first peak of the storm and remained low during the second peak of the storm (Fig. 3-4). This is different from a previous study that observed increasing concentrations of *Bacteroides* spp. gene copies over the course of a storm at coastal sites (Converse et al., 2011). This may be due to the differences in the climate and landscape, which result in different hydrologic responses. For example, the storms in this study lasted less than 24 hr, while the storms in the study of Converse et al. (2011) lasted approximately 80 hr with four or five peaks in each hydrograph.

Overall, concentrations generally peaked slightly earlier than the hydrograph, suggesting rapid inputs into the stream after the onset of precipitation. Concentrations did not typically decrease with discharge during the duration of the storm, while the intra-storm loading rates generally follow the hydrograph more closely. The difference between these two measures is critical from a watershed management perspective. The bulk of water-quality literature has focused on concentrations of indicators because the primary historical concern with regard to microbial water-quality has been public health risks related to direct contact between swimmers and surface waters at recreational sites (e.g., beaches) (Schoen and Ashbolt, 2010; Soller et al., 2010). However, it is important to note that in small urban streams, the primary concern is typically not direct human contact with water; instead, it is their role in transporting fecal contaminants to larger water bodies downstream where human exposure risks are more likely. In this case, or any time water-quality

management is considered from a whole watershed or system perspective, consideration of loads rather than concentrations is critical in understanding system behavior (Badgley et al., 2011). To improve the accuracy of load estimations, multiple samples spanning the whole hydrograph with higher frequency during the rising limb should be employed if possible, instead of existing single grab sampling at regular (e.g., monthly or seasonally) frequencies. Calculating loading rates of fecal indicators, rather than simply reporting concentrations, is critical for identifying the most prominent sources across all spatial and temporal scales in a watershed.

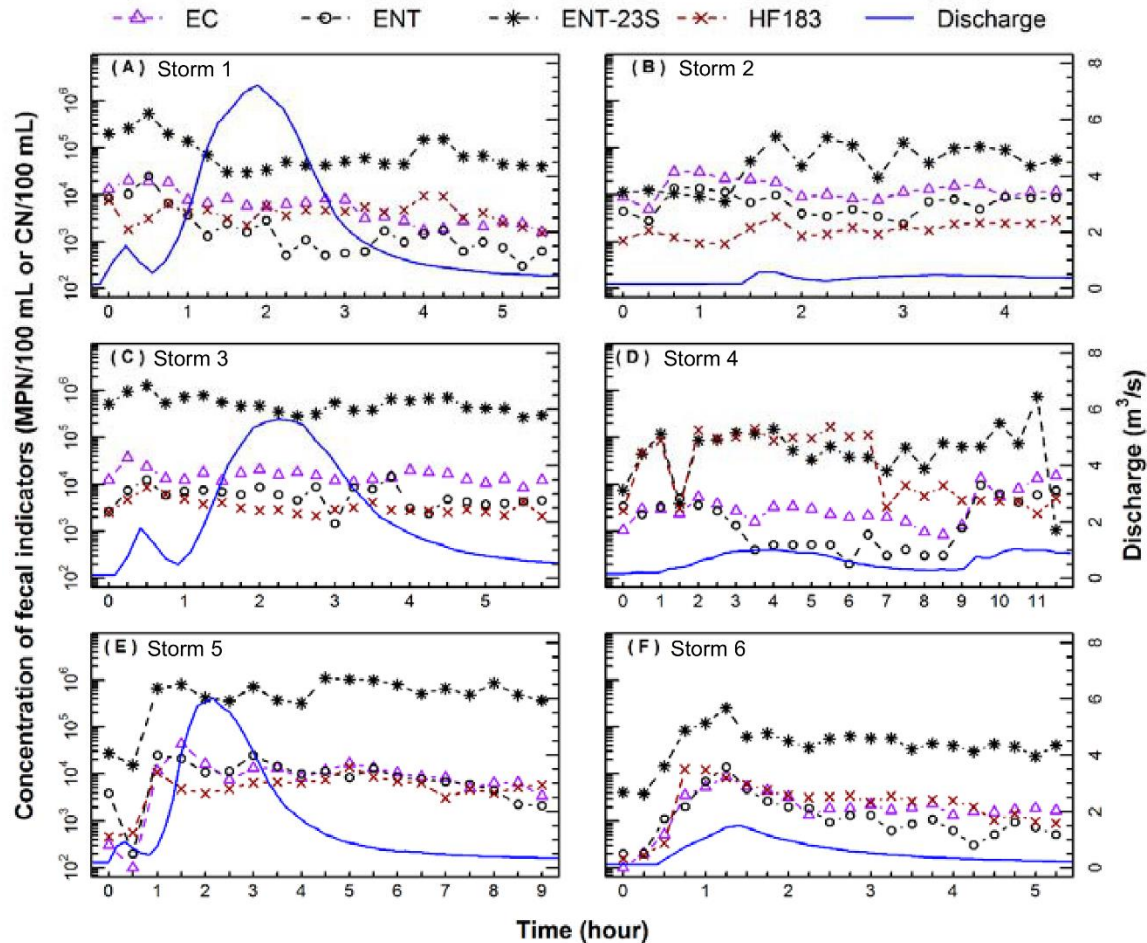


Figure 3-3. Intra-storm patterns of concentrations of each fecal indicator (X-axis represents hours passed since the beginning of each storm event).

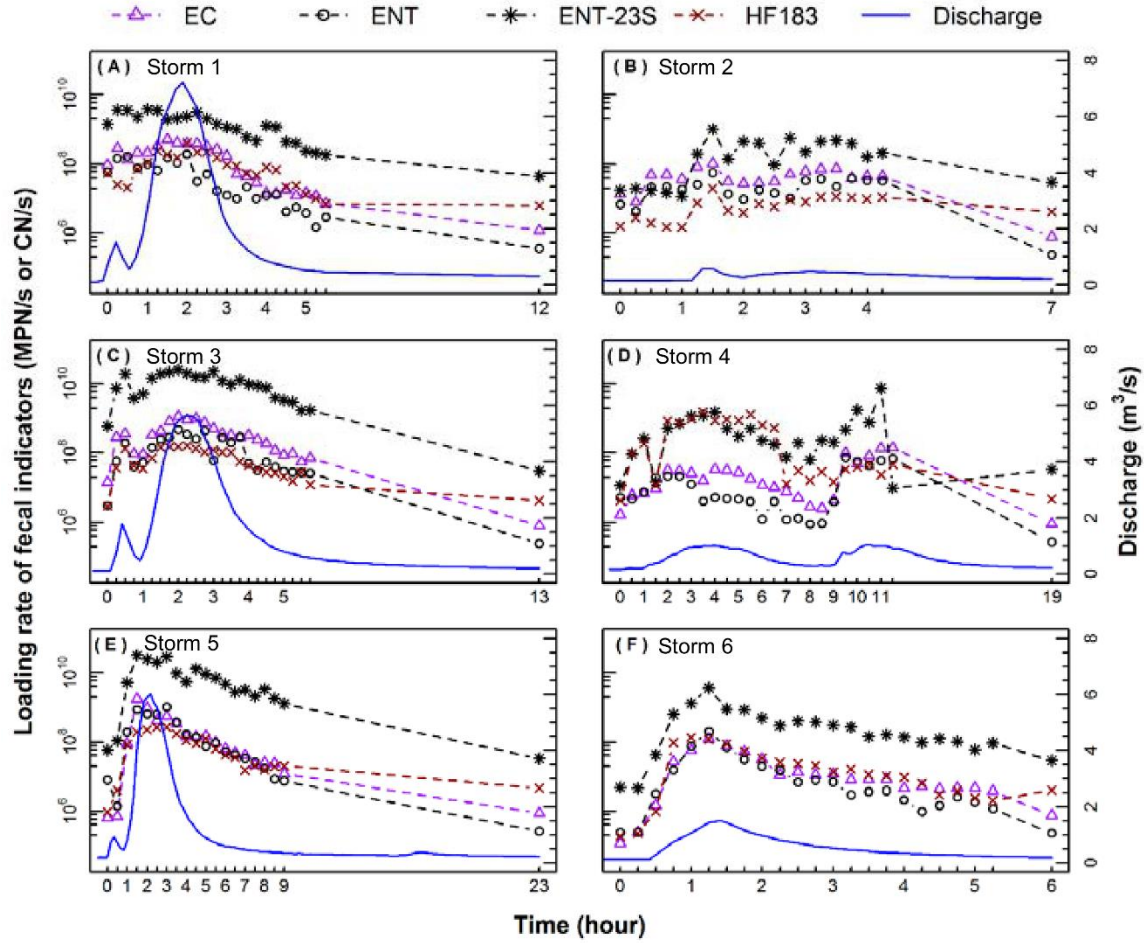


Figure 3-4. Instantaneous loadings rate of each fecal indicator during storm events (X-axis represents hours passed since the beginning of each storm event; the average of dry-weather samples were used to estimate the instantaneous loading rate corresponding to the end of each storm)

3.3.3. Relationships between the FIB concentrations measured by different methods

PCA on the complete dataset of concentrations of the four fecal indicators (EC, ENT, ENT-23S and HF183, $n=137$) resulted in most of the data variance (79.4%) being contained in the first two components, PC1 and PC2 (Fig. 3-5). The correlation circle describes the correlations between each variable and the two components, with the angle between two arrows representative of the correlation of the respective variables; there is no linear dependence if the angle is 90° , while an

angle greater than 90° indicates a negative correlation (Husson et al., 2014). EC, ENT and ENT-23S were most important variables for PC1 ($r=0.88$, 0.86 , 0.78 respectively; $p<0.001$), while HF183 was the most important variable for PC2 ($r=0.93$, $p<0.001$). EC, ENT and ENT-23S were closely correlated with each other as indicated by the narrow angles between each arrows, while showing weak correlations with HF183 (Fig. 3-5). This makes sense given that EC, ENT, and ENT-23S are associated with all fecal sources in the watershed, while HF183 is generally associated with human sources. These observations agree with data from coastal areas with weak or no correlations between culturable FIB concentrations and qPCR measures of the human *Bacteroidales* genetic marker (Sauer et al., 2011; Gonzalez et al., 2012). In addition to variation in source, a lack of correlation may also result from different fate and transport processes. Therefore, existing watershed-scale models based on culturable *E. coli* may not be sufficient to predict source-specific genetic markers of fecal contamination. As emerging MST markers become integrated into water-quality monitoring efforts, additional research on the ecology of these targets in natural environmental systems will be critical to understand and predict their performance.

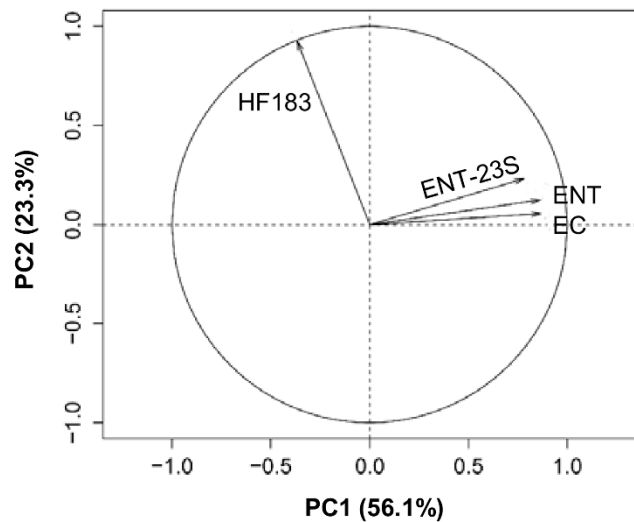


Figure 3-5. Variables factor map of PCA on the concentrations of the four fecal indicators.

3.3.4. Event load, equivalent background period, and association with key environmental variables

Event load (EL) represents the cumulative magnitude of total fecal inputs associated with a storm event, while equivalent background period (EBP) represents the number of time periods equal to the duration of the storm that would be required to transport the same load during dry-weather. Overall, the event loads of the *Enterococcus spp.* 23S rRNA marker were significantly higher than the event loads of culturable enterococci (Wilcoxon test, $p < 0.05$, Fig. **Error! Reference source not found.**3-6A), whereas EBPs associated with the qPCR measures were smaller (Wilcoxon test, $p < 0.05$, Fig. 3-6B). This corresponds to concentrations of the *Enterococcus spp.* 23S rRNA marker that averaged 130-times higher than corresponding culturable enterococci measures in dry weather, but only 60-times higher during storm events. This may reflect larger relative quantities of recently lysed cells or cells in a viable but not culturable state due to extended ultraviolet exposure during dry-weather periods. In contrast, during wet-weather flows, a substantial amount

of fresh fecal material is washed from the watershed surfaces into the stream, perhaps with lower quantities of stressed cells. Values for EBP of HF183 were generally even lower (except for storm 4, Fig. 3-6B), which may indicate a more substantial dry-weather source (e.g., constant sewage intrusion) that only modestly increased during storm events (e.g., flushing of storm sewer system). If these data truly represent human fecal contamination, these results are consistent with what would be expected from sewage intrusion, which would predominate in dry weather and be flushed during storm events. For all markers, the results of this work echo previous observations that total microbial loads from individual storms can be equivalent to loads transported during several months to a year of dry-weather (Krometis et al., 2007). Therefore, monitoring efforts aiding in remediation plans such as the TMDL program should target storm events in addition to dry-weather monitoring.

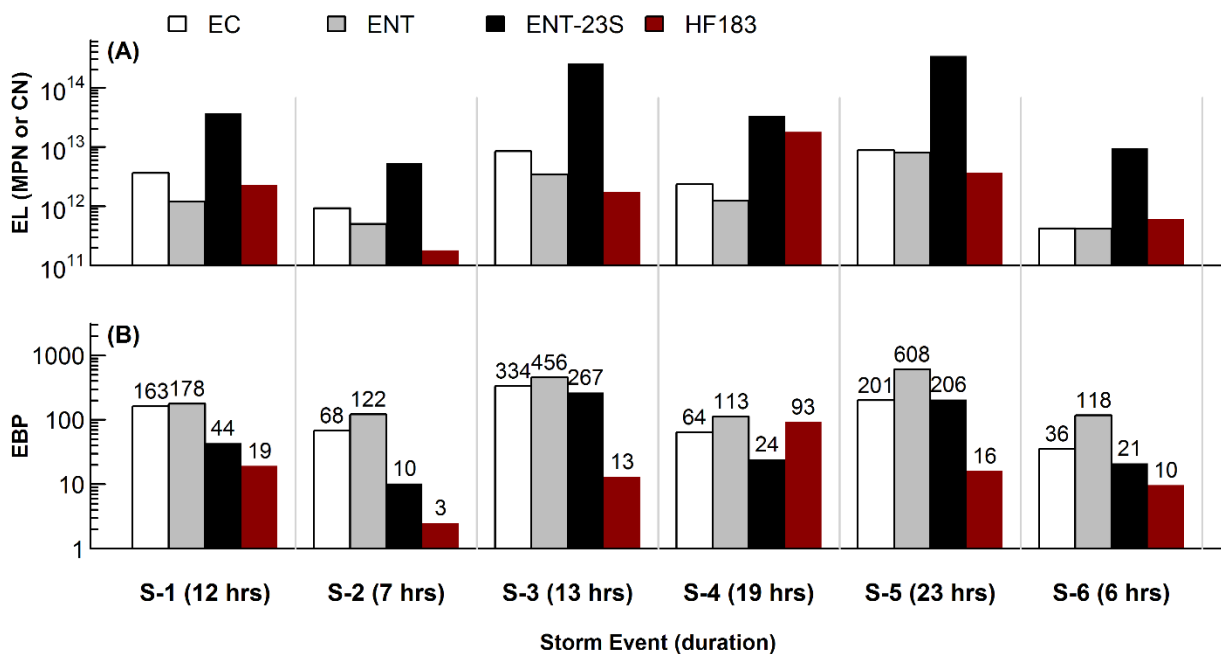


Figure 3-6. Measures of (A) event load (EL) and (B) equivalent background period (EBP) for each fecal indicator during each storm event.

PCA was performed on the complete dataset with event loads of the four fecal indicators (EC, ENT, ENT-23S rRNA and HF183) and selected environmental variables that show statistical significant correlation (Table S2) with event load of at least one of the four fecal indicators. Most of the data variance (80.7%) was contained in the first two components, PC1 and PC2 (Fig. 3-7). More importantly, the important environmental variables associated with the event loads of each fecal indicators were identified via the correlation circle (Fig. 3-7). The event loads of each of the four fecal indicators show moderate positive associations with runoff duration (R_v), total precipitation in each storm (P_T), and antecedent 7-day precipitation (AP_{7d}), but were negatively associated with minimum dissolved oxygen (DO_{min}). Environmental variables most strongly positively associated with the event loads of general fecal indicators (EC, ENT and ENT-23S) included total runoff volume (V), maximum turbidity (TB_{max}), and maximum flow (Q_{max}). In contrast, total event loads of HF183 were most strongly positively associated with time to peak flow (t_p) during a storm (Fig. 3-7).

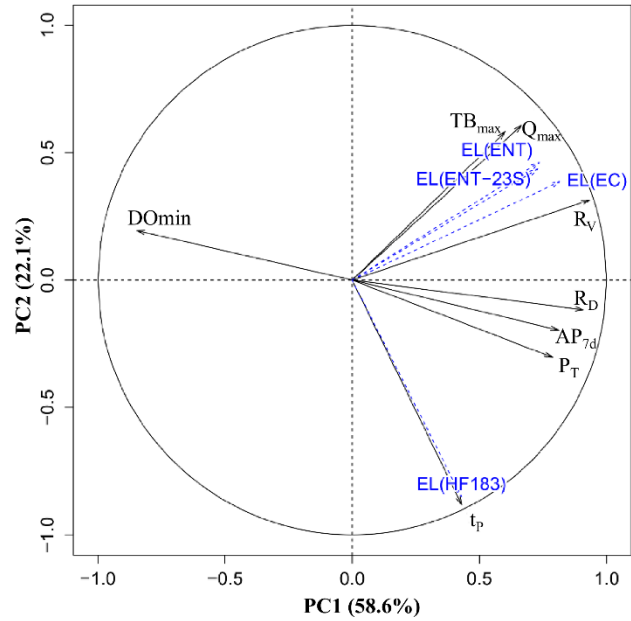


Figure 3-7. Variables factor map of PCA on the event loadings of the four fecal indicators and the environmental variables that showed statistical significant correlation with event loadings of at least one of the four fecal indicators (Table S2).

This study highlight the similarities and differences between storm loads of one source-specific MST marker and general fecal indicators during urban wet-weather flows. The results suggest that indicator source, rather than type (i.e., viable cell vs. genetic markers), may be a stronger determinant of transport process for fecal indicators. Given that human fecal contamination is generally considered to present more severe human health risks than other sources (Soller et al., 2010), and that urbanization, growing populations, and climate change can create more chances for exposure and dissemination, there is a critical need to improve understanding and prediction of transport processes for source-specific fecal indicators. Ideally, future water-quality models will incorporate these advances, e.g., more accurate identification of non-point sources of fecal contamination via microbial source tracking techniques, improved load estimation of fecal contamination via higher-frequency sampling techniques, and more appropriate fate and transport pathways and parameters for relating upstream to downstream concentrations.

Supporting information

Table S1. Hydro-meteorological and physicochemical variables used in correlation analyses.

Variable name	Description
Antecedent climatic variables that can indicate growth and removal on watershed surfaces	
Rad _x (x=1, 2, 7, 14, 28 days)	Mean net radiation (MJ/m ²) for x days prior to a storm event
AP _x (x=1, 2, 7, 14, 28 days)	Total precipitation (mm) in antecedent x days of a storm event
T _x (x=1, 2, 7, 14, 28 days)	Minimum temperature (°C) for x days prior to a storm event
Rainfall variables that can indicate microbial wash-off	
P _T	Total precipitation (mm) in a storm event
P _D	Precipitation duration of a storm event (hr)
P _I	Mean precipitation intensity of a storm event (mm/hr)
Stream flow variables that can indicate in-stream transport	
R _V	Total runoff volume (m ³)
R _D	Runoff duration of a storm event (hr)
Q _{max}	Maximum flow rate (m ³ /s)
Q _{mean}	Mean flow rate (m ³ /s)
t _p	Time to peak flow (hr)
Physicochemical water-quality variables that can indicate source, growth and removal in the stream and watershed surfaces	
TB _x (x=mean, min, max)	Mean, minimum, maximum turbidity during a storm event (NTU)
pH _x (x=mean, min, max)	Mean, minimum, maximum pH during a storm event
DO _x (x=mean, min, max)	Mean, minimum, maximum dissolved oxygen during a storm event (mg/L)

Table S2. Pearson's correlation coefficient between event loadings of each fecal indicator and environmental variables (p<0.1). All variables were log10-transformed to introduce log-normal distribution.

Environmental variables (log10- transformed)	Event loadings of fecal indicators in log10(CFU)			
	EC	ENT	ENT-23S	HF183
Total precipitation (mm) in antecedent 7 days of each storm event (AP _{7d})	0.71	0.78	0.70	0.81
Total precipitation (mm) of each storm event (P _T)	0.75			0.81
Total runoff volume (m ³) of each storm event (R _V)	0.90	0.85	0.90	0.73
Runoff duration (hr) of each storm event (R _D)	0.82	0.85	0.80	0.84
Maximum observed flow (m ³ /s) during each storm event (Q _{max})	0.76	0.71	0.80	
Time to peak flow (hr) of each storm event (t _p)				0.92
Minimum observed dissolved oxygen (mg/L) during each storm event (DO _{min})	-0.86	-0.73	-0.83	
Maximum observed turbidity (NTU) during each storm event (TB _{max})		0.77	0.75	

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Chapter 4. Long-term impacts of bacteria-sediment interactions in watershed-scale microbial fate and transport modeling

A research article submitted to Journal of Environmental Quality (March 2015):

Liao, H., L. Krometis, K. Kline, W. C. Hession, Long-term impacts of bacteria-sediment interactions in watershed-scale microbial fate and transport modeling. J. Environ. Qual.

Abstract

Elevated levels of fecal indicator bacteria (FIB) remain the leading cause of surface water-quality impairments in the United States. Under the Clean Water Act, basin-specific Total Maximum Daily Load (TMDL) restoration plans are responsible for bringing identified water impairments in compliance with applicable standards. Watershed-scale model predictions of FIB concentrations that facilitate the development of TMDLs are associated with a great deal of uncertainty relative to other water-quality contaminants. An increasingly cited criticism of existing modelling practice is the common strategy that assumes bacteria behave similarly to “free-phase” contaminants, i.e. bacteria-sediment interactions are neglected, though substantial field evidence indicates a nontrivial number of cells do preferentially associate with particulates. Only limited attempts have been made to evaluate the impacts of sediment on the predictions of in-stream FIB concentrations at the watershed-scale, and limited observational data is available for model development, calibration, and validation. This study aims to evaluate the impacts of bacteria-sediment interactions in a continuous, watershed-scale model (Hydrological Simulation Program - Fortran, or HSPF) widely used in TMDL development. In addition to observed FIB concentrations in the water column, streambed sediment-associated FIB concentrations were available for improved model calibration. Overall, while improved model performance was achieved as compared to previous studies, model performance under a “sediment-attached” scenario was essentially equivalent to the simpler “free-phase” scenario commonly employed in TMDL development. Watershed-specific characteristics (e.g. steep slope, high imperviousness) likely contributed to the dominance of wet-weather associated pollutant loading in the water column, which may have obscured sediment impacts. Site evaluation preceding modeling efforts is necessary to determine

whether the additional model complexity and effort associated with partitioning phases of FIB is sufficiently offset by gains in predictive capacity.

4.1. Introduction

Pathogen contamination, typically assessed via elevated levels of fecal indicator bacteria (FIB, e.g. *Escherichia coli* or *E. coli*, enterococci, fecal coliforms), remains the leading cause of surface water-quality impairments in the United States (USEPA, 2015). Considering the wide range of designated uses precluded or otherwise impacted by unacceptable FIB levels, including recreation, irrigation, aquaculture, and drinking, this represents a potentially huge economic loss (Collier et al., 2012). Identified water impairments are primarily addressed through the development of basin-specific Total Maximum Daily Load (TMDL) restoration plans in accordance with the sections 303(d) and 305(b) of the US 1972 Clean Water Act (CWA) (USEPA, 2015). The bacterial TMDL process is particularly notable for the considerable expense involved; cost estimates range from \$4,000 to \$1,000,000 per TMDL developed, not including subsequent implementation (Birkeland, 2001). As watershed-scale models are extensively employed during the TMDL processes to estimate the relative contributions of pollutant sources and to evaluate the effectiveness of potential remediation strategies, continuing model refinement to incorporate emerging scientific knowledge is critical to improve the efficiency and prioritization of remediation efforts.

Unfortunately, due to a limited understanding of microbial fate and transport in the environment, predictions of FIB concentrations by watershed-scale models are associated with a great deal of uncertainty relative to other water-quality contaminants (Novotny, 2003, Benham et al., 2011). Existing modeling practice commonly assumes bacteria behave as “free-phase” contaminants with

near-neutral buoyancy, i.e. governed only by die-off and transport downstream with the bulk flow (Jamieson et al., 2004). However, several studies note that stream bed sediments can harbor 10 to 10,000 times more FIB than the overlying water column in a variety of aquatic environments (Buckley et al., 1998, An et al., 2002, Pandey et al., 2012, Liao et al., 2014). In addition, bacteria can be released and resuspended into the water column if bottom sediments are disturbed (Jamieson et al., 2005, Cho et al., 2010, Pandey et al., 2012). Sediment-attached FIB appear to survive for extended periods due to the local abundance of nutrients and physical protection from protozoa and Ultraviolet light (Garzio-Hadzick et al., 2010, Droppo et al., 2011), potentially posing an extended period of human health risk (Droppo et al., 2011). Not surprisingly, many reviews of the TMDL process emphasize the need to develop and include more appropriate representations of bacteria fate and transport in watershed-scale models (NRC, 2001, Ferguson et al., 2003, Benham et al., 2006).

A number of studies have successfully included bacteria-sediment interactions in mathematically modeling in-stream FIB during experimental conditions or short-term storm events (Bai and Lung, 2005, Jamieson et al., 2005, Rehmann and Soupir, 2009, Cho et al., 2010, Droppo et al., 2011, Guanghai et al., 2011). In contrast, very few studies have attempted to link sediment and microbial transport using watershed-scale models over long time periods, which will be of greatest use to watershed managers concerned with TMDL development and the long-term attainment of water-quality goals to support designated uses. Kim et al. (2010) modified the Soil and Water Assessment Tool (SWAT) through the addition of a streambed *E. coli* release and deposition module, and calibrated using one-year of observational data of *E. coli* concentrations in both the water column and bed sediments. These efforts resulted in better agreement between predicted and observed in-

stream *E. coli* concentrations as quantified by the Nash-Sutcliffe Efficiency or NSE value (average improvement from -90 to -0.2). Russo et al. (2011) incorporated microbial-sediment association into the Hydrological Simulation Program - Fortran (HSPF) model to simulate bacterial transport in an urbanized watershed using existing model subroutines. The model was calibrated using one-year of observational data of in-stream fecal coliform concentrations, but no field observations of sediment concentrations of coliform were available. Though this added effort improved model performance, the impacts were quite minimal, which was attributed to the dominance of wet weather watershed microbial loads. A subsequent sensitivity analysis supported this assumption, indicating that given current knowledge of appropriate parameter ranges governing settling velocities, soil erodibility, partitioning coefficients, and die-off, variations within appropriate parameter ranges failed to change estimates of overall water FIB concentrations by more than 10%, i.e. upland loading to the receiving water remained dominant over concentrations from sediment. However, Russo et al. (2011) also noted that HSPF estimates of sediment FIB concentrations, which assume a uniform distribution throughout the stream reach in terms of length and depth, appeared crude in comparison to field observations, and required confirmation.

The overall goal of this study was to determine whether the inclusion of bacteria-sediment interactions within HSPF would improve downstream predictions of *E. coli* concentration. A primary limitation of the Russo et al (2011) study was the lack of sediment coliform concentrations for model calibration; these data are difficult to obtain as most water-quality monitoring programs only record water FIB concentrations. The present study targeted an urbanizing stream in Virginia (USA) where a paired sediment and water column FIB monitoring effort recently concluded (Liao et al., 2014). With this dataset, we aimed to: 1) augment HSPF with a bacteria-sediment-

association module; 2) calibrate the HSPF model parameters using both water column and bed sediment concentrations of *E. coli*; and 3) evaluate the potential significance of streambed *E. coli* release and deposition in long-term (2 year) simulations of daily in-stream *E. coli* concentrations using this augmented model, as compared to the traditional assumption that *E. coli* behave as dissolved constituents. By providing estimates of the relative significance of distinct bacteria fate and transport processes, we hope to facilitate the development of more accurate modeling strategies, which should improve TMDL effectiveness and efficiency.

4.2. Methods

4.2.1. Study area

Our study focuses on the 31 km² upper Stroubles Creek watershed within the Ridge and Valley ecoregion of Virginia, USA (Fig.4-1a). Land use within the watershed is primarily residential (48%), with additional land uses including forest (30%), pasture (18%), and cropland (4%) (Fig. 4-1b). Annual precipitation ranges from 910 mm to 1300 mm. Stroubles Creek is designated as a primary contact recreational water by the Commonwealth of Virginia and required to meet “fishable and swimmable standards” (VADEQ, 2015a), although it is worth noting that the observed depth at base flow does not exceed 33.5 cm (Abel, 2012). The creek runs approximately 15 km from the northeastern town of Blacksburg, via the Virginia Tech campus, and then into the New River, which has served as the region’s main source of drinking water since 1950 as well as home to a variety of recreational activities. An 8-km section of the stream was designated as in violation of the general biological integrity clause of the CWA due to degraded benthic macroinvertebrate ecology in 1996, with sediment identified as the primary stressor. A related sediment TMDL, including an implementation plan, was developed in the early 2000s (VADEQ

and VADCR, 2003, VADEQ and VADCR, 2006). In addition, an 11-km reach segment (the 8-km reach segment with benthic impairment plus an additional 3-km reach segment downstream) was more recently listed for violation of the *E. coli* standard, with a TMDL to reduce the *E. coli* levels currently required (VADEQ, 2015a).

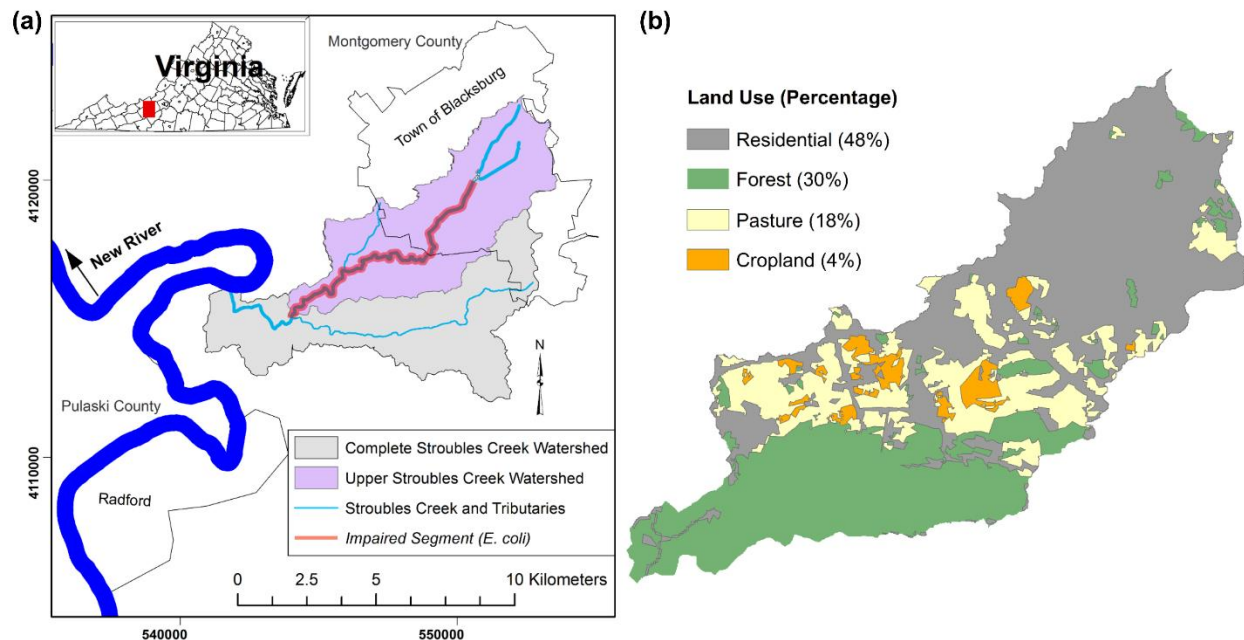


Figure 4-1. Location and land use of Stroubles Creek watershed (Virginia, USA)

4.2.2. Model development

The HSPF (version 12.2, Bicknell et al., 2005) was selected as a primary tool for this work, as it has been used extensively in efforts to support TMDL development to address bacteria impairments in keeping with requirements of the CWA (Benham et al., 2006). It is a continuous, deterministic, lumped-parameter, watershed-scale model that is supported by both USEPA and USGS. Although bacteria are most often modeled as a “free-phase” generalized water-quality constituent in HSPF during TMDL development efforts, HSPF does have the ability to model bacteria as a “sediment-attached” constituent (Bicknell et al., 2005). In previous efforts, HSPF

has been used to model contaminants like polychlorinated biphenyls (PCBs) and phosphorus, as both dissolved and sediment-attached phases to support USEPA-approved TMDL development (USEPA, 2010, Tetra Tech 2009).

4.2.2.1. Sub-watershed delineation and spatial data acquisition

The upper Stroubles Creek watershed boundary was delineated in ArcGIS 10.1 using the 10-m National Elevation Dataset (NED). Land use was acquired from the National Land Cover Database 2006 (NLCD 2006), and the stream network was obtained from the National Hydrography Dataset (NHD). Soil data was obtained from Soil Survey Geographic Database (SSURGO) of the USDA and NRCS. The watershed was divided into nine sub-watersheds based on local land use homogeneity, stream network continuity, and monitoring station locations to facilitate model calibration and validation. For modeling purposes, the stream was simplified such that there is only one stream segment within each sub-watershed (i.e. labeled from 1 to 9 from downstream to upstream, Fig.4-2).

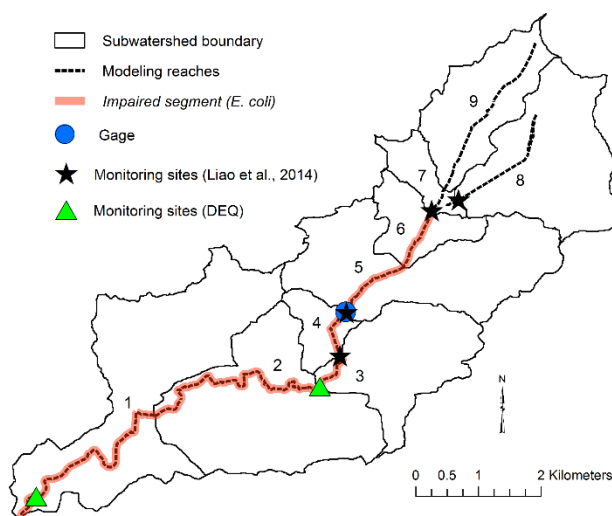


Figure 4-2. Upper Stroubles Creek watershed delineation, simplified reach segments and monitoring sites for modeling.

4.2.2.2. Hydrology module

Weather data were compiled from available stations within or near the watershed: daily minimum and maximum temperature were obtained from the National Climatic Data Center (NCDC) station at the Blacksburg National Weather Service Office (NWSO) (COOP ID: 440766); hourly precipitation data were obtained from Kentland farm, approximately 10 km from the watershed (<http://www.vaes.vt.edu/college-farm/weather/2014/weather2014.html>); and daily dew point temperature, average daily wind speed, and percent sun were obtained from the Lynchburg Regional Airport station, approximately 120 km away from the watershed, the closest station that records these data.

Stream stage is currently monitored and recorded at 15-min intervals by the Virginia Tech Stream Research, Education, and Management Laboratory (StREAM Lab) (Thompson et al., 2012), and is converted to flow rate via an existing stage-discharge equation developed using the velocity-area method (NRCS, 2014). The 15-min streamflow data were averaged to produce a daily dataset for hydrology calibration (period: 1/1/2012-12/31/2013) and validation (period: 1/1/2009-12/31/2011) of the HSPF model following the methods described in USEPA BASINS Technical Note 6 (USEPA, 2000).

4.2.2.3. Sediment module

Sediment loads and in-stream transport were modeled following the methods detailed in USEPA BASINS Technical Note 8 (USEPA, 2006). The watershed sediment loadings per unit area were calibrated for each land use to the values published in the previous sediment TMDL report for this site, which were estimated using the Universal Soil Loss Equation (VADEQ and VADCR, 2003).

In brief, HSPF simulates the transport, deposition and scour of sediment in a reach segment as functions of bed shear stress (Eq. 4-1):

$$\tau_b = SR\rho g \quad (4-1)$$

where τ_b = bed shear stress (N m^{-2}); S = slope (m m^{-1}); R = hydraulic radius (m); ρ = density of water (kg m^{-3}); and g = acceleration of gravity (m s^{-2}).

For the silt and clay size particles, the critical shear stress of deposition (τ_{cd}) and resuspension (τ_{cr}) for each size are adjusted so that the model calculates deposition during low flow periods, resuspension during high flow events, and transport with neither resuspension nor deposition for moderate flow rates. The rates of sediment deposition (R_d) and resuspension (R_r) are calculated as Eq. 4-2 and Eq. 4-3

$$R_d = v_s C_{ss} \left(1 - \frac{\tau_b}{\tau_{cd}} \right) (\tau_b < \tau_{cd}) \quad (4-2)$$

$$R_r = M \left(\frac{\tau_b}{\tau_{cr}} - 1 \right) (\tau_b > \tau_{cr}) \quad (4-3)$$

where v_s = quiescent water settling velocity (m d^{-1}); C_{ss} = suspended-sediment concentration (kg m^{-3}); M = erodibility coefficient ($\text{kg m}^{-2} \text{d}^{-1}$).

4.2.2.4. Bacteria module

For consistency's sake, water-quality modeling was conducted with fecal coliform inputs, and then a translator equation was used to convert the output to *E. coli* for the final results (VADEQ, 2003); this is the existing standard procedure employed by the Virginia Department of Environmental

Quality (VADEQ) for bacteria TMDL development. The watershed fecal coliform loads were estimated using the Bacteria Source Load Calculator (Zeckoski et al., 2005). The HSPF model was run separately under two scenarios: 1) a “free-phase” scenario, where bacteria are assumed to behave in a manner similar to dissolved-phase contaminants in keeping with current standard practice; and 2) a “sediment-attached” scenario, where a portion of bacteria are assumed to be associated with sediments. Under the “free-phase” scenario, advection and generalized first-order decay were simulated, and the model output included all “free-phase” *E. coli* in the water column. Under the “sediment-attached” scenario, advection and generalized first-order decay were simulated for “free-phase” and “sediment-attached” *E. coli* separately. Additional processes modeled under the “sediment-attached” scenario included adsorption/desorption between *E. coli* and sediment given a linear reversible isotherm, and streambed *E. coli* resuspension and deposition as a function of sediment resuspension and deposition, which are detailed in a previous study (Russo et al., 2011). Estimates of model parameters affecting microbial fate and transport are summarized in Table 4-1. Model outputs of in-stream *E. coli* concentrations in the “sediment-attached” scenario are the sum of “free-phase” and “sediment-attached” *E. coli* in the water column. Assuming *E. coli* are primarily associated with fine sediments (i.e., silt and clay), the in-stream *E. coli* concentrations under this assumption can be calculated via Eq. 4-4.

$$C_{EC,water} = C_{EC,free} + C_{EC,clay}C_{ss,clay} + C_{EC,silt}C_{ss,silt} \quad (4-4)$$

Where $C_{EC,water}$ = concentration of *E. coli* in the water column (CFU L⁻¹); $C_{EC,free}$ = concentration of free-phase *E. coli* (CFU L⁻¹); $C_{EC,clay}$ = concentration of *E. coli* attached on the suspended clay particles (CFU mg⁻¹); $C_{EC,silt}$ = concentration of *E. coli* attached on the suspended silt particles

(CFU mg⁻¹); C_{ss,clay} = concentration of suspended clay particles (mg L⁻¹); C_{ss,silt} = concentration of suspended silt particles (mg L⁻¹).

Table 4-1. Estimates of model parameters affecting microbial fate and transport.

	Silt	Clay
Sediment parameters		
Diameter (μm) ^a	7.6	2.5
Density (g cm ⁻³) ^a	2.3	2.0
Settling velocity (cm sec ⁻¹) ^a	1.3 × 10 ⁻³	1.3 × 10 ⁻⁴
Critical shear stress for deposition (N m ⁻²) ^{a,b}	0.67	0.57
Critical shear stress for resuspension (N m ⁻²) ^{a,b}	2.68	2.25
Erodibility factor (kg m ⁻² day ⁻¹) ^a	0.01	0.01
Bacteria parameters		
Partition coefficient (L mg ⁻¹) ^c	0.5	0.5
Decay rate, free (day ⁻¹) ^d	1.15	1.15
Decay rate, suspended-sediment-associated (day ⁻¹) ^e	0.6	0.6
Decay rate, bed-sediment-associated (day ⁻¹) ^e	0.2	0.2

^aEstimated following methods provided in USEPA (2006).

^bCritical shear stress values for R5, detailed reach-specific shear stress modeling results were provided in (Appendix C)

^cEstimated such that attached *E. coli* fractions were 0.2 at background conditions and 0.5 during storms, consistent with previous studies (Characklis et al., 2005, Russo et al., 2011).

^dEstimated following methods provided in VADEQ (2003)

^eEstimates consistent with previous studies (Jamieson et al., 2004, Russo et al., 2011).

Multiple sources of water-quality data were available to assist in model calibration and validation. Water column concentrations of *E. coli* have been monitored at two sites by the VADEQ seasonally since 1980 (Fig. 4-2). Additionally, *E. coli* concentrations in both the water column and bed sediment were monitored weekly from February 2012 through January 2013 at four sites (Fig. 4-2) as described by Liao et al. (2014). The model calibration and validation periods were selected to include at least one dry year and one wet year. Depending on the data availability for each site (Fig. 4-2) during each period, the calibration and validation were conducted from the upstream sites to downstream sites. Finally, the simulated in-stream *E. coli* concentrations were calibrated to the observed values for the period of 1/12/2012-12/31/2013 (calibrated sites: R1, R4, R5, R7 and R8), and validated for the period of 1/1/2010 – 12/31/2011 (validated site: R1).

Under “sediment-attached” scenario, the simulated streambed *E. coli* concentrations were also calibrated to the observed values (calibrated sites: R4, R5, R7 and R8). It is worth noting that the observed *E. coli* concentration in the bed sediments were measured at the outlet of each sub-watershed, whereas the simulated values represented average values over the whole reach in each sub-watershed. This lumped-parameter approach assumed that the each divided reach was completely homogenous, which remains the only practical methodology, although *E. coli* concentrations in the bed sediments have been observed to vary substantially (Droppo et al., 2009, Badgley et al., 2011, Liao et al., 2014).

The performance of the calibrated and validated models were evaluated based on the simulation results for the period of 1/1/2009 – 12/31/2010 for sites R1 and R3. To account for the uncertainties in the time of sampling and a rainfall event during a day, a 3-day window approach as described in Russo et al. (2011) was used, and the closest model prediction from the day of, the day before, or the day after an observation was compared to the observed *E. coli* concentrations. Although this strategy can be criticized as providing an overestimation of model accuracy, it is considered a standard practice in modeling waterborne microorganisms given the great deal of uncertainty and variability associated with monitoring (Benham et al., 2006, McCarthy et al., 2008, Russo et al., 2011)

4.3. Results

4.3.1. Hydrology calibration and validation

In keeping with best modeling practice, the Nash-Sutcliffe Efficiency (NSE) was used to quantitatively evaluate the agreement between simulated and observed flow following hydrology

calibration and validation (Moriassi et al., 2007). Final NSE values for the calibration and validation periods were 0.62 and 0.51, respectively, which is in keeping with satisfactory values reported in the literature (Moriassi et al., 2007, Seong et al., 2015). This calibrated and validated hydrology module provided the basis for *E. coli* predictions under both “free-phase” and “sediment-attached” scenarios.

4.3.2. Calibration and validation of in-stream *E. coli* concentrations under “free-phase” scenario

Initially, the water-quality module of HSPF was calibrated and validated under the “free-phase” scenario most commonly employed in bacterial modeling to support TMDL development, i.e. *E. coli* behave in a manner similar to dissolved contaminants and do not interact with particulates (Benham et al., 2006). During the calibration period, at least 96% of simulated *E. coli* concentrations were within one order of magnitude of observed values at all calibration sites (Fig. 4-3a-e), with a mean differences between observed and modeled values of less than 0.45 logs. Performance during the validation period was even higher (Fig. 4-3f): 100% of the simulated *E. coli* concentrations were within one order of magnitude of the observed values, and the mean difference was only 0.35 logs.

It is important to note that predictive modeling of in-stream bacteria concentrations at the watershed scale is very challenging due to the considerable variability associated with monitoring observations, as well as poor understanding of fate and transport behavior (Novotny, 2003, Benham et al., 2011). Earlier efforts consider a difference of one-order of magnitude between

simulated and observed results acceptable (Benham et al., 2006, Dorner et al., 2006), with typical reported mean differences ranging from 0.39 logs to 0.66 logs via a three-day window approach (Russo et al., 2011). Comparatively, the results in this study would be considered highly acceptable.

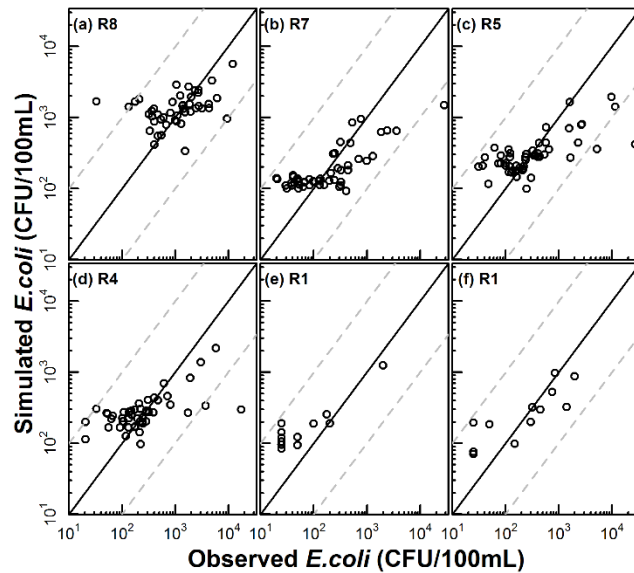


Figure 4-3. Simulated versus observed *E. coli* concentrations during the (a-e) calibration, and (f) validation period under the “free-phase” scenario. A three-day window approach was used to select the best modeling results from the day before, the day of, or the day following the observation. The black solid 1:1 line is equivalent to perfect agreement between the simulated and observed values; the grey dotted lines represent a deviation equivalent to one-order of magnitude.

4.3.3. Calibration and validation of in-stream *E. coli* concentrations under “sediment-attached” scenario

Given the unique monitoring dataset available, *E. coli* concentrations in both the streambed sediment and overlying water column could be calibrated to observed values under the “sediment-attached” scenario, though it is worth noting underlying difficulties. Because HSPF simply provides a total *E. coli* load for the entire reach’s bed sediment (in CFU), these values had to be

converted to average point concentrations prior to comparison with observation values by dividing the simulated total mass of bed sediment in that specific reach (in CFU/mg). Therefore, the horizontal and spatial variations of streambed *E. coli* concentrations were not accounted for in this study. Parameters were adjusted such that the simulated streambed *E. coli* concentrations were mostly (R8: 93%, R7: 92%, R5: 86% and R4: 92%) within one-order of magnitude of the observed values (Fig.4-4).

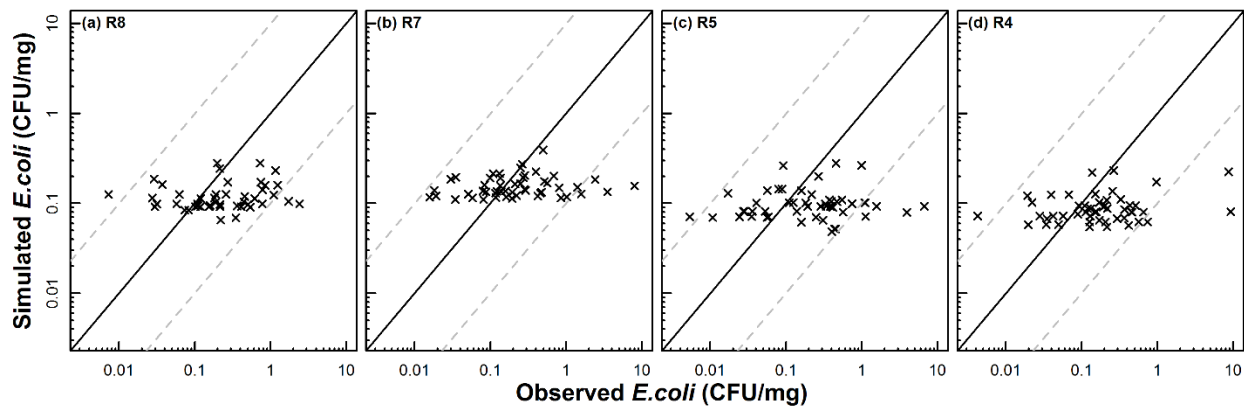


Figure 4-4. Comparison of simulated and observed *E. coli* concentrations in streambed sediment. A three-day window approach was used to select the best modeling results from the day before, the day of, or the day following the observation. The black solid 1:1 line is equivalent to perfect agreement between the simulated and observed values; the grey dotted lines represent a deviation equivalent to one-order of magnitude.

Parameter values associated with streambed *E. coli* concentrations remained constant while calibrating (Fig. 4-5a-e) and validating (Fig. 4-5f) the in-stream *E. coli* concentrations under the “sediment-attached” scenario. During the calibration period, at least 92% of simulated *E. coli* concentrations were within one order of magnitude of observed values at all calibration sites. The mean differences between observed and modeled values varied from 0.33 logs to 0.58 logs for the five calibration sites. During the validation period, 92% of the simulated *E. coli* concentrations were within one order of magnitude of the observed values, with a mean difference of 0.5 logs.

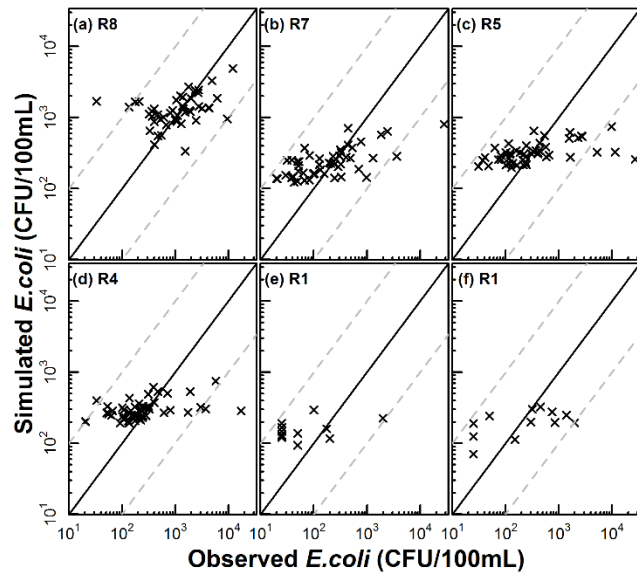


Figure 4-5. Simulated versus observed *E. coli* concentrations during the calibration (a-e) and validation (f) period under “sediment-attached” scenario. A three-day window approach was used to select the best modeling results from the day before, the day of, or the day following the observation. The black solid 1:1 line is equivalent to perfect agreement between the simulated and observed values; the grey dotted lines represent a deviation equivalent to one-order of magnitude.

4.3.4. Comparison of model performance under “free-phase” vs. “sediment-attached” scenario

To compare the performance of the two calibrated and validated scenarios, a third simulation period was subsequently explored (1/1/2009 – 12/31/2010). Performance was evaluated solely on the basis of agreement with *E. coli* concentrations in the water column in keeping with regulatory standards used to designate impairments. Under the “free-phase” scenario, 100% simulated in-stream *E. coli* concentrations were within one order magnitude of the observed values, with a mean difference of 0.25 logs for the upstream reach segment (R3, Fig. 4-6a) and 0.34 logs for the downstream reach segment (R1, Fig. 4-6b). Under the “sediment-attached” scenario, the percentage of simulated in-stream *E. coli* concentrations within one order magnitude of the

observed values was 92% for R3 and 100% for R1, with mean differences of 0.34 and 0.49 logs for R3 (Fig. 4-6a) and R1 (Fig. 4-6b) respectively.

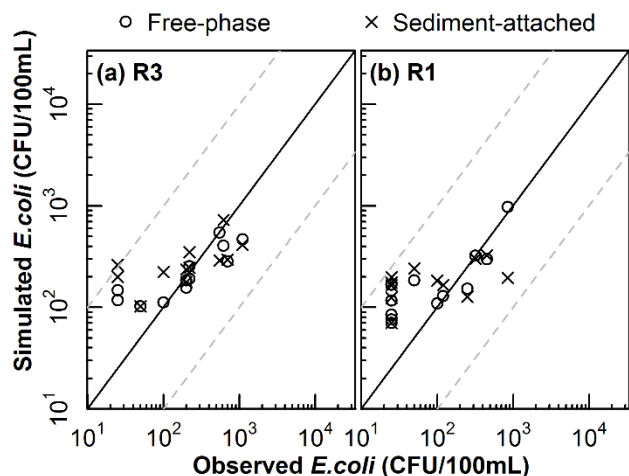


Figure 4-6. Simulated versus observed *E. coli* concentrations under "free-phase" scenario (circle symbols) and "sediment-attached" scenario (cross symbols) during the simulation period for R3 (a) and R1 (b). A three-day window approach was used to select the best modeling results from the day before, the day of, or the day following the observation. The black solid 1:1 line is equivalent to perfect agreement between the simulated and observed values; the grey dotted lines represent a deviation equivalent to one-order of magnitude.

4.4. Discussion

Outputs from watershed-scale hydrologic models used to predict FIB concentrations are associated with considerable uncertainty. Consequently, unlike nutrient or sediment concentrations, a prediction within one-order of magnitude of an observed value is generally considered acceptable. Regardless of "free-phase" or "sediment-attached" scenario, better performance, as measured by the percent predicted values within one-order of magnitude of observed values, was demonstrated in this study (90-100%) as compared to previous reported efforts (70-90%) (Dorner et al., 2006, Russo et al., 2011). The relatively large observational dataset for multiple calibration sites in this study likely contributed to these improvements.

In keeping with previous work by Russo et al. (2011), inclusion of a “sediment-attached” module in HSPF did not appear to appreciably change model outputs or overall performance, despite the availability of *E. coli* concentrations in the streambed sediment for calibration. Any observed differences were essentially negligible, given the considerable variation associated with any bacteria monitoring regime (McCarthy et al., 2008). Both the stream targeted by Russo et al. (2011) and this study’s Stroubles Creek are situated within urbanized watersheds with steep slopes (average slope in the present study: 12%), and prone to a “first flush” of overland contaminant loadings. Therefore, the wet-weather loading from the upstream watershed sources likely outweigh the impacts of release and resuspension from sediments on in-stream FIB concentration simulations, as demonstrated in the study of Ghimire and Deng (2013). More substantial impacts of the sediment on in-stream FIB concentration simulations would be expected at sites with gentle slope and low flow (e.g., a lake, or near a beach shore) (Thupaki et al., 2013).

One of the biggest advantages in this study was the inclusion of weekly observed *E. coli* concentrations in the bed sediments for model calibration. This represents a first attempt to use sediment *E. coli* concentrations to calibrate the HSPF model, although Kim et al. (2010) calibrated the modified SWAT using less frequently observed *E. coli* concentrations in the bed sediments (i.e. 25 observations over two years as opposed to 50 observations in one year in this study). Theoretically, and based on previous field evidence of bacterial resuspension, the magnitude of *E. coli* resuspended during high flows will be directly affected by the amount of *E. coli* available in the bed sediments, rendering calibration efforts on stream bed sediment *E. coli* concentrations of substantial importance to the reduction of model uncertainty. The negligible influence observed in this study could partly due to the dominance of wet-weather flow loadings, but also due to the

inability of HSPF to account for the heterogeneous distribution of *E. coli* in the stream bed sediment. Previous studies have suggested streambed *E. coli* concentrations can vary substantially with both depth and longitudinal distance (Bai and Lung, 2005, Kim et al., 2010, Badgley et al., 2011). While more detailed datasets for calibration are generally considered ideal, given the substantial labor and cost associated with *E. coli* monitoring as well as the added complexity of including sediment-calibration in model parameterization, it is worth considering whether these efforts are justifiable given the current realities of model development and practice. For lumped-parameter, watershed-scale models like HSPF, high-resolution data may not provide improvement, as modeled data inevitably represent the overall average of a reach segment, and are compared to averages over a substantial length of time (e.g. a three day window).

Ironically, although wet-weather loading eventually is generally identified as a primary source of microbial loading in developing watershed remediation plans (Gaffield et al., 2003), dry-weather periods may be more significant when considering public health risk, as these represent times when humans are more likely to engage in recreational use. Dry-weather periods may also prove to be the period of time when accurate model predictions of sediment release of bacteria reservoirs are most critical, as they would be expected to produce a much greater relative increase as compared to low base-flow concentrations of bacteria in an urbanized watershed. Future efforts to improve model accuracy through the incorporation of bacteria-sediment interactions are urged to examine dry-weather periods associated with public use patterns (e.g. summer) at a much finer time-scale (e.g. daily outputs) in order to identify conditions most likely to result in community health impacts and restrictions in appropriate designated uses.

4.5. Conclusion

Although considerable past research indicates that microbes are present in both a “free” and “sediment-attached” phase, there appears to be little demonstrable benefit, in terms of overall model performance, to the inclusion of separate phases in existing watershed-scale hydrologic models, even provided sediment-specific monitoring data to assist in parameterization. Limits in underlying model design (e.g. inability to account for spatial heterogeneity in reach sediments) and analytical uncertainties associated with microbial monitoring may limit model response. As wet weather loadings inevitably dominate calculations of in-stream FIB concentrations, given present model detail, the calculation of FIB load reductions associated with TMDL implementation plans will likely never be primarily attributed to the resuspension of sediment stores of FIB in urban watersheds. Careful consideration of site characteristics and intended applications (e.g. quantification of necessary overall load reductions versus identification of key periods of public risk) are key to determining whether the additional model complexity and effort associated with explicitly partitioning phases of microorganisms is sufficiently offset by gains in predictive capacity.

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Chapter 5. Human health risk estimation by coupling a continuous watershed-scale microbial fate and transport model with a stochastic model

A research article in preparation for submission to Risk Analysis:

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Abstract

Pathogen contamination indicated by elevated levels of fecal indicator bacteria (FIB) is the leading cause of surface water-quality impairments in the United States. The sufficiency of numerical compliance with FIB-based criteria as the endpoint of the existing watershed-specific Total Maximum Daily Load (TMDL) restoration plans is questioned by recent findings demonstrating poor correlations between FIB levels and the presence of actual human pathogens. Human illness risks associated with impaired surface waters have been estimated via a Quantitative Microbial Risk Analysis (QMRA) framework, but to date have focused on hypothetical watersheds and/or single events. This study is unique in that human illness risks were estimated within a QMRA framework by coupling a continuous watershed-scale fate and transport model (Hydrological Simulation Program – Fortran, or HSPF) with a stochastic dose-response model based on the USEPA “reference pathogens” approach. As HSPF is commonly used to assess watershed-level contaminant loads and reductions necessary to meet TMDL goals, this strategy could be readily incorporated into the TMDL process, providing greater clarity to stakeholders and watershed managers and potentially facilitating the development of more effective remediation efforts. QMRA results in our study watershed indicate that total human illness risks were consistently higher than the benchmark illness risk, even when the levels of FIB were in compliance. FIB from human sources was associated with the greatest illness risk relative to observations of concentration, and can increase dramatically during the occurrence of sanitary sewer overflows. Given recent research indicating sewer leakage are ubiquitous in urban areas that are not typically accounted for in the development of TMDLs, this is a particular concern, even in watersheds with separate storm and sewer systems. Uncertainty analysis indicated that more detailed site-specific

knowledge of pathogen presence and densities in each source was most likely to improve the accuracy of illness risk estimates.

5.1. Introduction

Pathogen contamination is the leading cause (14%) of surface water-quality impairments (USEPA, 2015), representing over 40,000 hospitalizations at a cost of \$970 million annually in the United States (Collier et al., 2012). Identified water impairments are primarily addressed through the development of basin-specific Total Maximum Daily Load (TMDL) restoration plans in accordance with the 1972 Clean Water Act's sections 303(d) and 305(b) (USEPA, 2015). During the TMDL processes, levels of fecal indicator bacteria ("FIB", e.g. *E. coli* and enterococci) are used to assess potential human health risks based on the assumption that FIB behave similarly to pathogenic organisms with respect to incidence, fate, and transport in the environment (Yates, 2007). Although TMDL development requires extensive hydrodynamics modeling of FIB concentrations over time, it is important to note that total (i.e. not source-specific) FIB concentration is predicted, and numerical compliance with relevant criteria remains the desired TMDL endpoint. The sufficiency of numerical compliance with FIB-based criteria has been questioned by several recent efforts that demonstrate: 1) poor correlation between FIB levels and pathogens/associated risks of human illness (Field and Samadpour, 2007, Wu et al., 2011, Harwood et al., 2014); 2) considerable differences between patterns of contamination in inland and surface waters, which renders broad application of standards developed based on epidemiology studies at sewage-impacted coastal sites less appropriate (Wade et al., 2003, Dorevitch et al., 2010); and 3) substantial variation in risks associated with FIB exposure between

sources (e.g. human vs. animal) (Schoen and Ashbolt, 2010, Soller et al., 2010, USEPA, 2010, Benham et al., 2011, Soller et al., 2014). Given the limited resources available, it is critical to prioritize remediation efforts through proper assessment of contamination levels and associated human health risks.

In response to these concerns, several recent studies have surveyed target surface waters directly for pathogens, in order to estimate human illness risks within a quantitative microbial risk analysis (QMRA) framework (McBride et al., 2013, Ishii et al., 2014, Sales-Ortells and Medema, 2014). QMRA is a mathematical strategy that can link environmental exposure to illness risk via epidemiological relationships (Haas et al., 2014). Given the time and expense associated with direct pathogen monitoring at the present time, and the number of waters that require protection, USEPA (2010) has proposed a “reference pathogens” approach to QMRA: a set of eight reference pathogens were established including *Norovirus*, *Rotavirus*, *Adenovirus*, *Cryptosporidium* spp., *Giardia lamblia*, *Campylobacter* spp., *Salmonella*, and *E. coli* O157:H7. These reference pathogens are generally considered representative of the fate and transport of other waterborne pathogens of concern, and have relatively established dose-response relationships based on extensive review of the scientific literature. This strategy has been applied to investigations of gastrointestinal illness (GI) risks posed by human recreational contact with a variety of waterbodies impacted by both human and animal sources. However, in all cases QMRA was conducted based on exposure during a limited period of time, i.e. there have been no attempts previously to apply this strategy over temporal or climatic changes in water-quality. While this is appropriate to short-term surface water management decisions (e.g. beach closures), long-term watershed remediation efforts (e.g. TMDLs) generally consider compliance and risk over multiple

years in conjunction with deterministic watershed models to determine appropriate interventions and societal investments.

The aim of this present study was to quantitatively estimate human health risk from exposure to waterborne pathogens by coupling an existing watershed-scale model widely used in TMDL development with a stochastic model via the reference pathogens approach in order to identify potential discrepancies in FIB levels and GI illness risks. It was hypothesized that because risk has proven highly source-dependent in previous studies (Schoen and Ashbolt, 2010, Soller et al., 2010, USEPA, 2010), periods of highest human health risk may not always coincide with periods of highest total FIB concentration. The specific objectives were to: 1) partition the simulated waterbody *E. coli* concentrations among major watershed sources with the HSPF model; 2) estimate pathogen human doses of pathogens by source; 3) quantify source-specific and total human illness risks over multiple years; and 4) compare violations of *E. coli*-based criteria and equivalent illness rate.

5.2. Methods

5.2.1. Study area

The study targets the 31-km² upper Stroubles Creek watershed within the Ridge and Valley ecoregion of Virginia, USA, which has been described extensively in previous work (Thompson et al, 2012, Liao et al., 2014). An 11-km segment of the Stroubles Creek is currently included on the 303(d) list of impaired waters due to violation of Virginia *E. coli* standards (SWCB, 2010), with a related TMDL to reduce *E. coli* levels required (VADEQ, 2015a). Official potential pollutant sources of concern include discharges from municipal separate storm sewer systems

(MS4), pet wastes, livestock (grazing or feeding operations), wet weather discharges, municipal (urbanized high density area), wildlife other than waterfowl, and other unspecified domestic waste (VADEQ, 2015a).

5.2.2. Modeling source-specific *E. coli* concentrations

Daily waterbody *E. coli* concentration outputs from a continuous watershed-scale model (Hydrologic Simulation Program – Fortran, or HSPF) for the entire period of 1/1/2010-12/31/2014 (see Chapter 4 and Appendix C for model details) were partitioned into four major pollutant sources: wildlife (duck and geese); livestock (cattle); domestic pets (dog), and human (failing septs and sanitary sewer overflows). Major pollutant watershed sources of concern were selected based on presence in this watershed and the availability of literature data for subsequent risk calculations. Other potential sources (e.g. raccoons, muskrats, deer, or pig slurry, etc.) were assumed to have negligible effects on the overall illness risk of the watershed (USEPA, 2010). Source-specific *E. coli* concentrations were obtained from HSPF by eliminating contributions from the other sources during each run (see Appendix C for detailed model modifications).

5.2.3. Quantitative microbial risk analysis (QMRA)

In order to link these source-specific outputs with risk via QMRA, a stochastic model (Fig. 5-1) was constructed in Analytica Professional Version 4.5.3 (Lumina Decision Systems, Inc., Los Gatos, CA, USA). A Monte Carlo simulation approach was used to capture the natural variability of the model input parameters, with 10,000 iterations per run. Median values from each of the 10,000 iterations were entered into R version 3.1.1 (R Development Core Team, 2013) for calculating and plotting the monthly median-GI illness risks. The importance analysis feature in

Analytica was used to identify which inputs contributed the most uncertainty to the estimation of illness risks, which is evaluated based on the absolute rank-order correlation between each input sample and output sample.

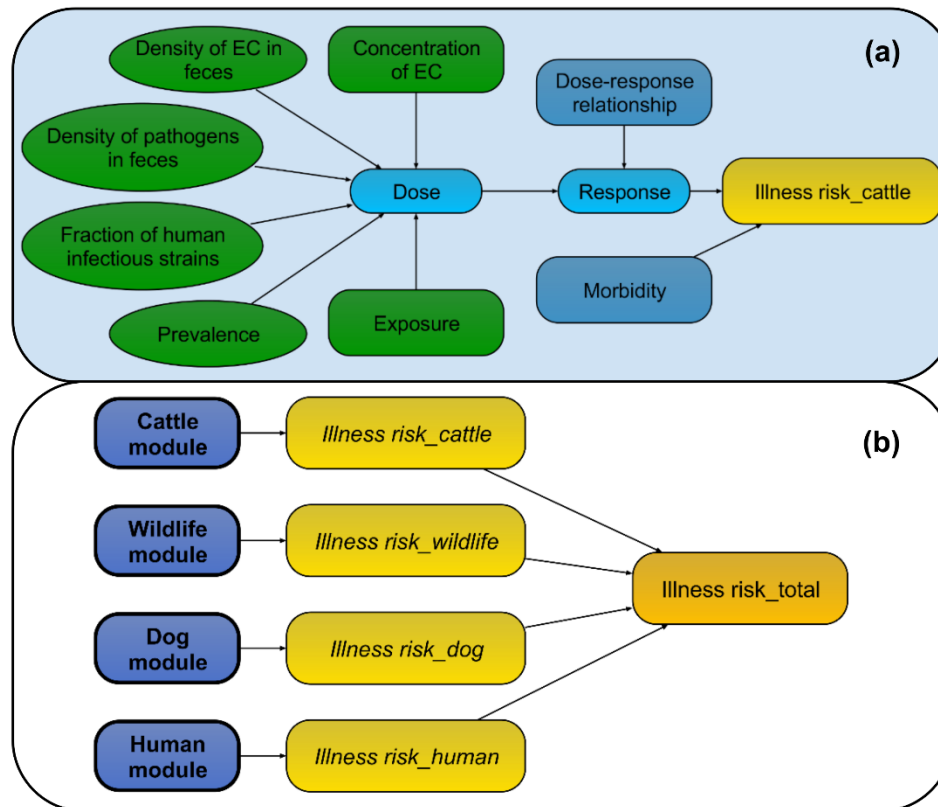


Figure 5-1. Stochastic model construction in Analytica: (a) example module for illness risk from cattle; (b) overall model for total illness risk calculation

5.2.3.1. Selection of reference pathogens

Reference pathogens were selected based on recommendations from USEPA (2010) and potential pollutant sources in this specific watershed. Six reference pathogens were included in this study: *Campylobacter jejuni*, *E. coli* O157:H7, *Cryptosporidium* spp., *Giardia lamblia*, *Salmonella enterica*, and norovirus.

5.2.3.2. Estimation of source-specific pathogen doses

The dose of each reference pathogen from each source was estimated as a function of source-specific FIB densities in the water as detailed in Eq. 5-1, which is a method similar to those used in previous QMRA studies of surface water (Schoen and Ashbolt, 2010, Soller et al., 2010, USEPA, 2010).

$$\mu_{rp}^S = \frac{c_{FIB}}{100} \times \frac{R_{rp}^S}{F_{FIB}^S} \times p_{rp}^S \times I_{rp}^S \times V \quad (5-1)$$

where S is the FIB source (i.e. livestock, human, dog, and bird), μ_{rp}^S is the dose of each reference pathogen from each source (CFU or oocysts), c_{FIB} is the concentration of FIB in water body (CFU 100mL⁻¹), R_{rp}^S is the density of reference pathogen in source feces (CFU or oocysts g⁻¹), F_{FIB}^S is the density of FIB in source feces (CFU g⁻¹), p_{rp}^S is the fraction of human-infectious pathogenic strains from source S, I_{rp}^S is the prevalence of infection in the non-human source (proportion of animals shedding the pathogen), and V is the volume of water ingested (mL).

The reference pathogens corresponding to cattle and human sources and their associated parameters for dose estimation were in keeping with previously published studies (Schoen and Ashbolt, 2010, Soller et al., 2010, USEPA, 2010). However, two additional sources not previously targeted were identified as critical for Stroubles Creek: wildlife (geese and duck), and dog feces. *Campylobacter jejuni* was selected as a reference pathogen for wild waterfowl and dog, as previous studies have suggested a high background prevalence of this pathogen in these animals (Fallacara et al., 2001, Roser et al., 2006, Ogden et al., 2009, Colles et al., 2011, Moriarty et al., 2011). In

addition, *Campylobacter jejuni* is a well-established zoonotic organism that has received considerable recent concern (Murphy et al., 2005, Moriarty et al., 2012). The values of each of the model input parameters in Eq. 5-1 are summarized in Table 5-1. The volume of water ingested was modeled as a log-normal distribution (median: 2.92, geometric standard deviation: 1.43) following previous studies (Dufour et al., 2006, Schoen and Ashbolt, 2010, Soller et al., 2010). When calculating dose of cattle manure, a 30-day storage time was applied following the similar method as described in Soller et al. (2014). The die-off rates (k , d^{-1}) used were 0.05 for *E. coli* in cattle manure (Soupir et al., 2008), 0.1 for *Salmonella* and *Campylobacter* (USEPA, 2010), and 0.07 for *E. coli* O157:H7 (USEPA, 2010).

Table 5-1. Summary of input parameters to calculate dose.

C_{FIB}	F_{FIB}^S (log ₁₀ range, CFU/g)	Reference Pathogen	R_{rp}^S (log ₁₀ range, Pathogens/g)	p_{rp}^S	I_{rp}^S	Reference(s)
HSPF output (cattle)	5.0 – 6.7	<i>Campylobacter jejuni</i>	1.2-7.3	67%-100%	5-38%	(Soller et al., 2010)
		<i>E. coli</i> O157:H7	3.1-8.4	67%-100%	9.7-28%	
		<i>Cryptosporidium</i> spp.	2.3-3.9	67%-100%	0.6-23%	
		<i>Giardia lamblia</i>	0-4.9	67%-100%	0.2-37%	
		<i>Salmonella enterica</i>	3-5.8	33-66%	5-18%	
HSFP output (duck)	2.5-8.5	<i>Campylobacter jejuni</i>	1.7-6	33-66%	13.4-38.3%	(Ogden et al., 2009, Meerburg et al., 2011, Moriarty et al., 2011)
HSPF output (geese)	2.0-8.1	<i>Campylobacter jejuni</i>	2-5.6	33-66%	14.7-35.5%	(Ogden et al., 2009, Meerburg et al., 2011, Moriarty et al., 2011)
HSPF output (dog)	6.9-8.1 ^a (EC: 6.3, 7.4)	<i>Campylobacter jejuni</i>	3-6	33-66%	0-46%	(Cox et al., 2005, Ogden et al., 2009, Chaban et al., 2010)
HSPF output (human)	6.7-8.0	<i>Norovirus</i>	3-6	100%	100%	(Soller et al., 2010)

Note values shown are minimum and maximum of log₁₀-uniform distributions unless otherwise specified (e.g. 5.0 corresponds to 10^{5.0})

a. Values represented fecal coliform densities in dog feces, which were converted to *E. coli* densities for dose estimation via the USEPA recommended equation: *E. coli* = 0.98814866*(Fecal coliform^{0.91905}).

5.2.3.3. Converting dose to risk of GI illness

The infection probability for a healthy adult resulting from accidental ingestion of impaired recreational water was calculated by feeding the pathogen doses to corresponding dose-response relationships from the literature (Table 5-2). Subsequently, the risk of GI illness (conditional on infection) for each pathogen from source S (P_{ill}^{RP}) was calculated by multiplying the probability of infection and the morbidity data from the literature (Table 5-2). The distribution of GI illness risk from each source (P_{ill}^S) and the total GI illness risk (P_{ill}) were calculated using Eq. 5-2 and Eq. 5-3, respectively.

$$P_{ill}^S = 1 - \prod_{RP} (1 - P_{ill}^{RP}) \quad (5-2)$$

$$P_{ill} = 1 - \prod_S (1 - P_{ill}^S) \quad (5-3)$$

Table 5-2. Dose-response relationships.

Does-response model	Reference pathogen	Parameter values	ID50 ^a	Morbidity ^b	References
Exponential $P_{inf} = 1 - e^{-rd}$	<i>Cryptosporidium</i> spp.	$\gamma = 0.09$	8 oocysts	50%	(Soller et al., 2010, USEPA, 2010, Soller et al., 2014)
	<i>Giardia lamblia</i>	$\gamma = 0.0199$	35 cysts	45%	
Beta-Poisson $P_{inf} = 1 - (1 + d/\beta)^{-\alpha}$	<i>Salmonella enterica</i>	$\alpha = 0.3126$ $\beta = 2884$	23600 cfu	20%	
	<i>E. coli</i> O157:H7	$\alpha = 0.248$ $\beta = 48.8$	207 cfu	28%	
	<i>Campylobacter jejuni</i>	$\alpha = 0.145$ $\beta = 7.59$	800 cfu	28%	
Hypergeometric $P_{inf} = 1 - {}_1F_1(\alpha, \alpha + \beta, -d)$	Norovirus	$\alpha = 0.04$ $\beta = 0.055$	1018 genome copies	60%	

a Median infectious doses; the dose that will infect 50% of exposed individuals. For exponential model, $ID_{50} = -\ln(\frac{1}{2})/r \approx 0.693/r$; For Beta-Poisson model, $ID_{50} \approx \beta(2^{1/\alpha} - 1)$; For hypergeometric model, ID50 must be obtained by finding the value of the average dose (d) satisfying the exact relationship: $P_{inf} = 1 - {}_1F_1(\alpha, \alpha + \beta, -d) = \frac{1}{2}$, where ${}_1F_1$ is the confluent hypergeometric function.

b Percentage of infections resulting in illness

5.3. Results and discussion

5.3.1. Comparing monthly geometric means of *E. coli* concentrations with associated GI illness risks

The monthly geometric means of daily waterbody *E. coli* concentrations were compared to the existing *E. coli* geometric mean Recreational Water-Quality Criteria (RWQC) of 126 CFU/100 mL (Fig. 5-2a). Overall, consistent standard violations occurred over the course of study period (85.4% of time). The largest source of waterbody *E. coli* concentrations was geese/duck, followed by livestock and dog. Contributions from human sources was consistently lowest, which is not surprising giving that the watershed has separate storm and sewer systems. For model input, an average rate of 5% of failing septic systems was applied to the houses that do not connect to sewer, which represent only 2.7% of all houses within the watershed. In addition, only 10 sanitary sewer overflows were reported over the four years (VADEQ, 2015b) that were input into the model as point sources. However, it is worth noting that contributions of *E. coli* from human sources may be an underestimate, as our previous study suggested high levels of molecular markers from human sources (see Chapter 3). This may reflect a common problem in the development of TMDLs at urban watersheds, where human sources are typically evaluated using a standard estimated number of straight pipes, failing septic systems, and reported sanitary sewer overflows only. Based on several recent studies (Sercu et al., 2008, Sauer et al., 2011), molecular markers indicating sewer leakage are ubiquitous in urban areas due to aging infrastructure. Quantifying source origins is critical to estimating illness.

Median monthly GI illness risks exceeded the RWQC equivalent illness risk (36/1000) for the entire study period, even when the levels of *E. coli* were in compliance (Fig. 5-2). GI illness risks associated with duck and geese contributions dominated the overall GI illness risks for the majority of the study period. It is worth noting that although the monthly geometric means of human-specific *E. coli* concentrations remained very low (Fig. 5-2a), reported sanitary sewer overflows dramatically increased risk of GI illness, at times by over two orders of magnitude (Fig. 5-2b). This is in agreement with previous studies that demonstrated higher illness risks for pathogens from human sources as compared to other sources under hypothetical conditions (Soller et al., 2010). Therefore, given the possibility of systematic underestimation of *E. coli* concentration from human sources in the Stroubles Creek watershed (see Chapter 3), the actual illness risks might be higher. Although primary contact and direct ingestion of water in this stream is unlikely given a water depth ranging from 13 cm to 33.5 cm during baseflow conditions (Abel, 2012), minimizing health risks is important to protecting downstream discharges into the New River, which is a regional source of drinking water and home to a variety of recreation activities (Parece et al., 2010).

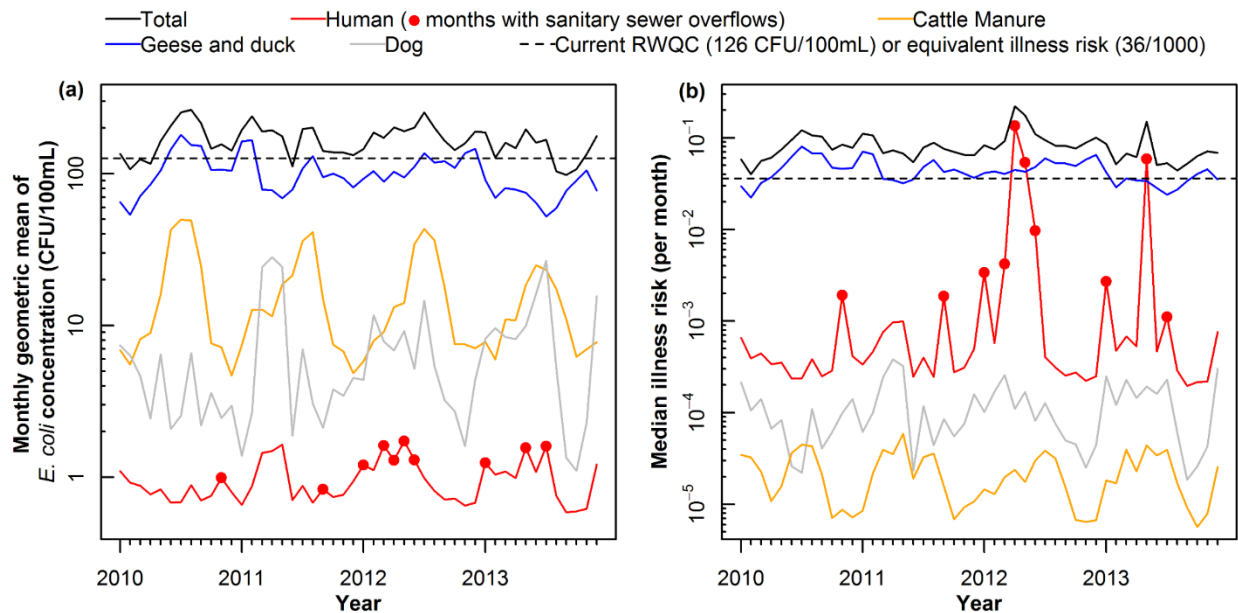


Figure 5-2. Contribution of *E. coli* concentrations and associated illness risk from each source. (a) Monthly geometric mean of *E. coli* concentrations and a comparison with the current geometric mean recreational water-quality criteria (RWQC) of 126 CFU/100mL *E. coli*; (b) median illness risks per month and a comparison with the current RWQC equivalent illness risk of 36/1000 (the median values from the 10,000 Monte Carlo simulations for each day were output to estimate the monthly illness risk via $1 - \prod_{month}(1 - P_{ill})$).

5.3.2. Importance and sensitivity analysis of stochastic input variables

In order to identify the parameters that are the primary contributors to the uncertainty in illness risk estimates, the importance of each variable is determined in Analytica by calculating the absolute rank-order correlation between each stochastic input variable and the resulting illness risk. This methodology is advantageous in that it is less sensitive to outliers and skewed distributions, and it works well even there are strong interactions between input variables (Lumina, 2014). Variables in the study model that have absolute rank-order correlation coefficient (r) greater than 0.5 were considered to have a significant impact on the estimation of illness risks (Lumina, 2014), and were summarized in Table 5-3. The sensitivity of each important variable was evaluated

by calculating the percent changes in illness risks associated with 1% increase in the important variables.

Table 5-3. Summary of importance and sensitivity of stochastic input variables

Source	Important variables ($r > 0.5$)	Sensitivity (mean $\pm$ sd ^a)
Duck and geese	Density of <i>E. coli</i> in duck feces	-0.27 $\pm$ 0.032
	Density of <i>E. coli</i> in geese feces	-0.31 $\pm$ 0.014
	Density of pathogen in duck feces	0.27 $\pm$ 0.032
	Density of pathogen in geese feces	0.31 $\pm$ 0.014
Human	Density of pathogen in sewage	1.00 $\pm$ 0.009
Dog	Density of pathogen in dog feces	1.00 $\pm$ 0.004
Cattle manure	Density of <i>E. coli</i> in cattle manure	-1.00 $\pm$ 0.002

^asd: standard deviation

The densities of *E. coli* and/or specific reference pathogens in the source feces were identified as of greatest importance to estimates of human illness risks (Table 5-3). Given the time and expense associated with establishment of a watershed-specific pathogen profile, densities of FIB and reference pathogens in source feces were typically assumed to follow log10-uniform distributions to account for the relatively wide range of possibilities reported in the literature in previous QMRA studies (Schoen and Ashbolt, 2010, Soller et al., 2010, USEPA, 2010, Soller et al., 2014). The variations of other input parameters were relatively smaller (Table 5-1). Consequently, given a certain percentage of change in input parameters, a greater change in illness risks would be expected to associate with *E. coli* and/or reference pathogens densities. As these parameters have also been identified as important in previous QMRA studies (Schoen and Ashbolt, 2010, USEPA, 2010), future research targeting improved quantification of these identified variables at specific sites would be critical to improve the accuracy of associated illness risk estimates.

5.4. Conclusion: risk management implications for urban watersheds

While previous studies have applied QMRA to estimate human health risks under idealized conditions (e.g. a hypothetical watershed with fixed sources of pollution, or a single time points, etc.), this present study is unique in that human health risks were estimated for a real urban watershed over a four-year period. By coupling a continuous watershed-scale microbial fate and transport model frequently used in existing TMDL processes with a study-specific stochastic model, a framework was provided to translate concentrations of *E. coli* (the existing TMDL targeted endpoint) into human illness risks, which can provide greater clarity to stakeholders and the general public, and perhaps direct more effective remediation strategies.

As observed in several previous studies, *E. coli* from human sources was associated with the greatest illness risk relative to observations of concentration, and can increase dramatically during sanitary sewer overflows. Given that recent source-tracking studies, including Chapter 3 of this dissertation, indicate that human sewage inputs to urban watersheds may be systematically underestimated due to widespread infrastructure leakage not typically accounted for in model development strategies, caution should be taken to accurately characterize fecal contamination from human sources during TMDL assessments.

The biggest source of fecal contaminants and illness risks found in this study is from duck and geese feces, which has not commonly been included in previous QMRA studies. Even following five years of watershed implementation of various best management practices (BMPs, e.g. stream fencing, dog waste pick up stations, and bioretention cells) to address a benthic impairment of Stroubles Creek, high levels of *E. coli* are consistently detected (Liao et al., 2014). As these

existing BMPs do not target wildlife (e.g. duck and geese), or in fact may serve as additional wildlife habitat, this is not surprising; however, it may be of concern, given that an increasing number of studies have identified duck/geese feces as a potential human health hazard (Meerburg et al., 2011, Moriarty et al., 2011). Although at a given level of FIB, human sources would probably contribute to a greater risk of human illness relative to fecal wastes from duck and geese, the actual risk of human illness would depend on the magnitude of fecal wastes from human relative to duck and geese in a specific watershed. As no real feasible or effective mitigation strategies are available for controlling fecal wastes from duck/geese, it appears most reasonable to prioritize the control of fecal wastes from human sources (e.g. identify and fix aging and leaking infrastructures).

It is important to note that several simplifications and health-protective assumptions were made to facilitate the completion of a QMRA study for this watershed. The reference pathogens approach assumes the selected reference pathogens are representative of the fate and transport of all waterborne pathogens of potential health concern across all geographic regions. A relatively wide range of variables corresponding to each reference pathogen were derived from the literature, and a Monte Carlo simulation approach was used to account for the variability. In addition, median values from each Monte Carlo simulation were used to describe illness risks, and thus, risks associated with extreme, rare or low probability events were not counted. Another important assumption was the exposure scenarios. Although full-body recreational contact is unlikely in this specific stream, the volume of water ingested was assumed to follow a log-normal distribution as similar to previous studies (Schoen and Ashbolt, 2010, Soller et al., 2010), which would probably be inappropriate beyond the illustrative purposes. Nevertheless, the results of this study provide

important insight on the discrepancy in the source contributions to FIB levels and human illness risks, which would facilitate the development of more effective remediation plans.

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Chapter 6. Conclusions

Pathogen contamination, typically quantified by elevated levels of fecal indicator bacteria (FIB), remains the leading cause of surface water-quality impairments in the United States and a global public health concern. Understanding microbial fate and transport in the natural environment is critical for the design of effective and efficient remediation strategies (e.g. the Total Maximum Daily Load, or TMDL program in the United States). However, the complexity of microbial fate and transport mechanisms, together with inherent variability of the natural systems, render it extremely challenging to rigorously quantify these processes for implementation in predictive watershed-scale models. This study observed streambed sediments that harbored 40 to 350 times the *E. coli* concentrations of the overlying water column, and 7 to 580 times the enterococci concentrations of the overlying water column, which is in agreement with many previous studies and highlights the potential for substantial sediment storage of FIB. Major hydrometeorological and physicochemical variables influencing concentrations of FIB in both the water column and bed sediments included antecedent 24-h rainfall, stream water temperature, and dissolved oxygen. In addition, a comparison of observations in our study with several previous studies indicates that variables often considered general indicators of non-point source pollution (e.g. turbidity, flow) may not be universally applicable surrogates for FIB levels in all watershed types.

While several studies have successfully included sediment impacts in modeling in-stream FIB concentrations under experimental conditions or short-term storm events, very few studies have attempted to evaluate sediment impacts on the long-term predictions of in-stream FIB concentrations using watershed-scale models. The high spatio-temporal monitoring data of FIB

concentrations in both the water column and bed sediments collected by the first phase of this study enabled a more highly refined calibration of HSPF (a model commonly used in TMDL development). This resulted in overall better model performance as compared to previous studies (i.e. 90-100% versus 70-90% predicted values within one-order magnitude of observed values). However, the model did not perform better under a “sediment-attached” scenario than under the conventional “free-phase” scenario. Specific watershed characteristics (e.g. steep slope, and high imperviousness) probably contributed to the dominance of wet-weather associated pollutant loading from upstream watershed sources, which dwarfed the effect of FIB release and resuspension from stream bed sediments. Careful site evaluation preceding modeling efforts would facilitate determination of whether the additional model complexity and effort associated with partitioning phases of FIB is sufficiently offset by gains in predictive capacity. It is worth noting that although wet-weather contributions are generally identified as the primary source of overall microbial loads in many types of receiving waters, dry-weather periods may be of greater public health concern as these periods represent times when humans are more likely to engage in recreational use and direct contact. Thus, future efforts to improve model accuracy through the incorporation of bacteria-sediment interactions are urged to examine dry weather periods associated with public use patterns (e.g. summer) at a much finer time-scale (e.g. daily), which will aid in the identification of conditions most likely to result in community health impacts and restrictions in appropriate designated uses.

Moderate to high levels of the human-specific HF183 *Bacteroides* 16S rRNA genetic marker were detected in high-frequency stormwater samples, which was surprising for an urban watershed with separate storm and sanitary sewers, but consistent with recent studies suggesting sewage intrusion

into storm sewers and urban streams is common given aging infrastructure. As fecal contamination from human sources is generally considered to present more severe human health risks as compared to other animal sources, and continuing urbanization, growing populations, and climate change can create more chances for exposure and dissemination, there is a critical need to develop or update strategies to properly identify and replace aging, leaking infrastructure. Ideally, future water-quality models will incorporate these advances, e.g., more accurate identification of non-point sources of fecal contamination via microbial source tracking techniques, improved load estimation of fecal contamination via higher-frequency sampling techniques, and more appropriate fate and transport pathways and parameters for relating upstream to downstream concentrations.

The Quantitative Microbial Risk Analysis (QMRA) framework presented can be readily integrated into the existing TMDL process to translate source-specific FIB concentrations output from HSPF model into human illness risks, providing more clarity to stakeholders and watershed managers. Median estimated illness risks were consistently higher than the USEPA suggested Recreational Water-Quality Criteria (RWQC) equivalent illness rate (36/1000), even when the monthly geometric mean of *E. coli* concentrations was in compliance. Concentrations of *E. coli* from human sources were relatively low, and yet were associated with great illness risk, which increases by several orders of magnitude following sanitary sewer overflows. Given that fecal inputs from human sources are often underestimated in urban watersheds, as demonstrated here by the detection of moderate to high levels of human-specific HF183 *Bacteroides* 16S rRNA genetic marker in Stroubles Creek (Chapter 3), caution should be taken in assigning load allocations and reductions for urban watersheds (e.g. integrating the emerging microbial/chemical source tracking techniques into existing standard source evaluation strategies based solely on GIS spatial analysis).

Fecal contaminants from duck and geese represented a considerable human illness risk relative to other sources. Existing Best Management Practices (BMPs) like fencing streams, dog waste pick up stations and bio-retention cells would not be expected to reduce fecal inputs from duck and geese appreciably. Due to the lack of site-specific parameter values, the QMRA process is associated with considerable uncertainty. Improved quantification of the presence and distribution of reference pathogens at a specific site (e.g. density of *E. coli* and pathogens in source feces) would greatly improve the estimation of illness risks. Reductions in uncertainty would likely enhance buy-in from stakeholders and regulators in accepting and employing QMRA strategies in watershed remediation planning.

By focusing on a highly instrumented urban watershed, a wealth of high-resolution data were available for this study. However, data scarcity is much more common due to limited resources. Studies focusing on data-rich experimental watersheds allow in-depth understanding of complex environmental problems, and potentially provide a practical means for rapid problem identification and/or potential solutions to similar watersheds with less available monitoring data. Lessons from this study include:

1. Intensive data collection on streambed sediment FIB levels may not always be justified, given that the considerable effort involved in monitoring FIB levels in streambed sediments resulted in minor change in the model accuracy in this study. Higher-frequency observational FIB levels in the water column (e.g. weekly vs. monthly, multiple monitoring stations vs. a single station) would more efficiently contribute to the improvement of model accuracy.

2. While a complex mechanistic watershed-scale model (HSPF) was used in this study, simpler empirical models linking statistical relationships between FIB levels with other hydrometeorological and physicochemical variables may more efficiently fill short-term needs. The establishment of these empirical statistical models would require high-frequency monitoring data over multiple years (e.g. at least one dry year and one wet year) to account for variations in climate/hydrology.
3. Accurate identification and characterization of upland pollutant sources is the key to effective and efficient TMDL restoration efforts, and deserves priority investment. The source identification methodology (based on GIS spatial analysis of geographic and census data) most commonly used in existing TMDL process can be improved by integrating emerging Microbial Source Tracking (MST) techniques. While GIS-based methodology is beneficial as a first-screening to explore potential pollutant sources, MST techniques are more powerful in confirming the relative contributions of major pollutant sources of concern.
4. In addition to documenting FIB levels, identifying and monitoring pathogens of concern in a particular water body (e.g. investigating available epidemiological data) should be an ultimate goal if substantial human exposure and risk of disease is expected. The uncertainty associated with QMRA strategies is greatly increased due to a lack of understanding of pathogen levels. Therefore, developing and standardizing high-throughput and economically feasible methodologies for pathogen detection require significant future research efforts to ensure public health protection.

Appendix A: Weekly FIB monitoring Data

Raw data for weekly water column and streambed sediment FIB concentrations (02/2012-01/2013) at the five sites along the Stroubles Creek.

FIB concentrations in the water column:

Date	Site	Analyte	Positive Wells			Concentration (MPN/100mL)		
			Large	Small	Volume	Mean	95% Lower CI	95% Upper CI
2/6/2012	DPout	Coliforms	49	46	50	3972.6	2444.1	6600.5
2/6/2012	B1	Coliforms	49	23	50	821.2	521.2	1237.8
2/6/2012	B2	Coliforms	49	21	50	730.8	463.9	1110.9
2/6/2012	B3	Coliforms	49	18	50	615.2	390.5	942.5
2/6/2012	DPout	<i>E. coli</i>	49	22	50	774.6	491.7	1134.1
2/6/2012	B1	<i>E. coli</i>	42	10	50	221.2	162	297.5
2/6/2012	B2	<i>E. coli</i>	35	8	50	144.5	103	192.8
2/6/2012	B3	<i>E. coli</i>	42	10	50	221.2	162	297.5
2/6/2012	DPout	Enterococci	37	7	50	155.1	110.6	209
2/6/2012	B1	Enterococci	16	4	50	47.6	29.3	71.5
2/6/2012	B2	Enterococci	18	0	100	21.8	13.4	33.9
2/6/2012	B3	Enterococci	19	2	100	25.9	16.4	39.1
2/13/2012	DPout	Coliforms	47	12	50	344.7	239	484.4
2/13/2012	B1	Coliforms	41	7	50	191.9	136.8	260.9
2/13/2012	B2	Coliforms	44	8	50	237.5	169.3	325.3
2/13/2012	B3	Coliforms	46	5	50	250	173.3	353.7
2/13/2012	DPout	<i>E. coli</i>	19	2	50	51.8	32.9	78.2
2/13/2012	B1	<i>E. coli</i>	15	1	50	37.4	21.5	60
2/13/2012	B2	<i>E. coli</i>	30	4	50	100.8	69.9	140.2
2/13/2012	B3	<i>E. coli</i>	31	3	50	102.4	71	143.4
2/13/2012	DPout	Enterococci	6	1	50	14.8	6.5	28.8
2/13/2012	B1	Enterococci	4	1	100	5.2	1.8	10.8
2/13/2012	B3	Enterococci	2	0	100	2	0.3	7.1
2/27/2012	DPout	Coliforms	49	23	50	821.2	521.2	1237.8
2/27/2012	B1	Coliforms	48	16	50	456.4	316.4	646.2
2/27/2012	B2	Coliforms	48	15	50	437.4	303.3	629.1
2/27/2012	B3	Coliforms	48	10	50	357.8	248.1	515.6
2/27/2012	DPout	<i>E. coli</i>	13	4	50	38.9	23.2	60.9
2/27/2012	B1	<i>E. coli</i>	31	7	50	116.1	82.8	158.9
2/27/2012	B2	<i>E. coli</i>	30	5	50	104.1	72.2	144.4
2/27/2012	B3	<i>E. coli</i>	22	0	50	56.4	35.8	84.5
2/27/2012	DPout	Enterococci	9	0	50	19.6	9.4	36.7
2/27/2012	B1	Enterococci	8	0	100	8.6	4.5	16.9
2/27/2012	B2	Enterococci	4	2	100	6.2	2.4	12.2
2/27/2012	B3	Enterococci	9	1	100	10.9	5.6	19.5
3/6/2012	DPout	Coliforms	49	35	50	1632.8	1100.2	2349.2
3/6/2012	B1	Coliforms	49	26	50	976.9	620.1	1442.9
3/6/2012	B2	Coliforms	49	15	50	522.5	341.9	796.9
3/6/2012	B3	Coliforms	49	18	50	615.2	390.5	942.5
3/6/2012	DPout	<i>E. coli</i>	32	9	50	128.9	91.9	174.6

3/6/2012	B1	<i>E. coli</i>	46	11	50	303	216	415.6
3/6/2012	B2	<i>E. coli</i>	23	7	50	79.3	53.4	110.7
3/6/2012	B3	<i>E. coli</i>	30	9	50	117.6	83.8	158.9
3/6/2012	DPout	Enterococci	16	5	100	25	15.9	37.1
3/6/2012	B1	Enterococci	0	2	100	2	0.3	5.6
3/6/2012	B2	Enterococci	1	0	100	1	0.1	5.5
3/6/2012	B3	Enterococci	2	2	100	4.1	1.2	9
3/12/2012	DPin	Coliforms	49	42	50	2599.3	1700.7	3793.1
3/12/2012	DPout	Coliforms	49	11	50	428.5	280.4	641.9
3/12/2012	B1	Coliforms	46	13	50	323.2	230.4	441.1
3/12/2012	B2	Coliforms	49	16	50	551	371.3	833.5
3/12/2012	B3	Coliforms	47	12	50	344.7	239	484.4
3/12/2012	DPin	<i>E. coli</i>	49	16	50	551	371.3	833.5
3/12/2012	DPout	<i>E. coli</i>	19	2	50	51.8	32.9	78.2
3/12/2012	B1	<i>E. coli</i>	39	5	50	162.5	115.9	222.8
3/12/2012	B2	<i>E. coli</i>	47	10	50	321.4	222.9	452.7
3/12/2012	B3	<i>E. coli</i>	43	7	50	216.1	154.1	294.5
3/12/2012	DPin	Enterococci	6	2	100	8.4	3.7	15.3
3/12/2012	DPout	Enterococci	3	1	100	4.1	1.2	9.1
3/12/2012	B1	Enterococci	1	0	100	1	0.1	5.5
3/12/2012	B2	Enterococci	5	0	100	5.2	2.3	11.9
3/12/2012	B3	Enterococci	1	0	100	1	0.1	5.5
3/19/2012	DPin	Coliforms	49	47	50	4839.1	3260.7	9432.2
3/19/2012	DPout	Coliforms	49	42	50	2599.3	1700.7	3793.1
3/19/2012	B1	Coliforms	49	28	50	1095	716.5	1608.9
3/19/2012	B2	Coliforms	49	34	50	1540.2	1098	2188.1
3/19/2012	B3	Coliforms	49	36	50	1732.9	1167.7	2490.8
3/19/2012	DPin	<i>E. coli</i>	49	31	50	1297.6	849	1882.9
3/19/2012	DPout	<i>E. coli</i>	45	14	50	305.7	223.9	412.4
3/19/2012	B1	<i>E. coli</i>	49	17	50	581.9	380.7	892.1
3/19/2012	B2	<i>E. coli</i>	49	21	50	730.8	463.9	1110.9
3/19/2012	B3	<i>E. coli</i>	49	18	50	615.2	390.5	942.5
3/19/2012	DPin	Enterococci	48	35	100	549.3	402.3	724.5
3/19/2012	DPout	Enterococci	14	2	100	18.5	11	29.2
3/19/2012	B1	Enterococci	6	0	100	6.3	2.9	13.7
3/19/2012	B2	Enterococci	1	1	100	2	0.3	5.9
3/19/2012	B3	Enterococci	2	0	100	2	0.3	7.1
3/26/2012	DPin	Coliforms	49	35	25	3265.6	2200.5	4698.4
3/26/2012	DPout	Coliforms	49	45	25	6931.6	4670.7	10837.9
3/26/2012	B1	Coliforms	49	43	25	5654.4	3699.7	8406.5
3/26/2012	B2	Coliforms	49	39	25	4185	2820	6036.1
3/26/2012	B3	Coliforms	49	33	25	2908	1902.7	4195.5
3/26/2012	DPin	<i>E. coli</i>	39	6	25	334.4	238.4	455.3
3/26/2012	DPout	<i>E. coli</i>	37	8	25	319	227.4	427.8
3/26/2012	B1	<i>E. coli</i>	49	29	25	2317.7	1516.5	3388.7
3/26/2012	B2	<i>E. coli</i>	49	19	25	1302.2	826.6	1992.3
3/26/2012	B3	<i>E. coli</i>	48	10	25	715.6	496.2	1031.1
3/26/2012	DPin	Enterococci	14	7	100	24.5	16	36.1
3/26/2012	DPout	Enterococci	9	6	100	16.4	9.5	26.4
3/26/2012	B1	Enterococci	6	2	100	8.4	3.7	15.3
3/26/2012	B2	Enterococci	10	2	100	13.2	7.1	22
3/26/2012	B3	Enterococci	35	4	100	64.4	44.6	88.6
4/2/2012	DPin	Coliforms	49	42	25	5198.6	3401.4	7586.2
4/2/2012	DPout	Coliforms	46	11	25	606.1	432	831.2

4/2/2012	B1	Coliforms	48	17	25	952.9	660.7	1363.1
4/2/2012	B2	Coliforms	48	15	25	874.9	606.6	1258.2
4/2/2012	B3	Coliforms	47	12	25	689.3	478	968.9
4/2/2012	DPin	<i>E. coli</i>	49	26	25	1953.8	1240.2	2885.8
4/2/2012	DPout	<i>E. coli</i>	7	0	25	29.8	14.2	59.5
4/2/2012	B1	<i>E. coli</i>	28	1	25	164.1	110.6	235.2
4/2/2012	B2	<i>E. coli</i>	29	2	25	179.2	120.7	253.4
4/2/2012	B3	<i>E. coli</i>	28	3	25	176.5	122.4	250.1
4/2/2012	DPin	Enterococci	2	0	100	2	0.3	7.1
4/2/2012	DPout	Enterococci	1	0	100	1	0.1	5.5
4/2/2012	B1	Enterococci	7	1	100	8.5	3.9	15.6
4/2/2012	B2	Enterococci	1	0	100	1	0.1	5.5
4/2/2012	B3	Enterococci	10	1	100	12.1	6.5	21.1
4/9/2012	DPin	Coliforms	49	37	25	3683.4	2482	5128
4/9/2012	DPout	Coliforms	49	14	25	992.4	649.3	1487.6
4/9/2012	B1	Coliforms	47	15	25	767.2	546.9	1058
4/9/2012	B2	Coliforms	48	15	25	874.9	606.6	1258.2
4/9/2012	B3	Coliforms	48	12	25	774	521.5	1117.8
4/9/2012	DPin	<i>E. coli</i>	44	8	25	475	338.6	650.6
4/9/2012	DPout	<i>E. coli</i>	7	2	25	38.4	17.6	67.7
4/9/2012	B1	<i>E. coli</i>	22	1	25	118.2	75	175.9
4/9/2012	B2	<i>E. coli</i>	14	2	25	74	44	116.9
4/9/2012	B3	<i>E. coli</i>	18	4	25	107.4	68.2	159.2
4/9/2012	DPin	Enterococci	32	21	100	87.5	65.8	111.8
4/9/2012	DPout	Enterococci	0	1	100	1	0	3.7
4/9/2012	B1	Enterococci	16	1	100	20.1	12.4	31.8
4/9/2012	B3	Enterococci	2	1	100	3	0.7	7.4
4/16/2012	DPin	Coliforms	49	36	25	3465.8	2335.3	4981.5
4/16/2012	DPout	Coliforms	47	10	25	642.8	445.7	905.4
4/16/2012	B1	Coliforms	49	31	25	2595.3	1698.1	3765.8
4/16/2012	B2	Coliforms	49	23	25	1642.3	1042.5	2475.7
4/16/2012	B3	Coliforms	49	22	25	1549.3	983.4	2268.2
4/16/2012	DPin	<i>E. coli</i>	28	3	25	176.5	122.4	250.1
4/16/2012	DPout	<i>E. coli</i>	5	0	25	20.8	9.2	47.8
4/16/2012	B1	<i>E. coli</i>	31	8	25	239.2	170.5	325.5
4/16/2012	B2	<i>E. coli</i>	29	4	25	191.9	133.1	268.7
4/16/2012	B3	<i>E. coli</i>	23	3	25	136.2	89.1	196.8
4/16/2012	DPin	Enterococci	49	34	100	770.1	549	1094
4/16/2012	DPout	Enterococci	1	0	100	1	0.1	5.5
4/16/2012	B1	Enterococci	21	4	100	31.8	20.8	46.4
4/16/2012	B2	Enterococci	20	2	100	27.5	17.5	41.2
4/16/2012	B3	Enterococci	10	1	100	12.1	6.5	21.1
4/25/2012	DPin	Coliforms	49	47	20	12097.9	8151.9	23580.5
4/25/2012	DPout	Coliforms	49	36	25	3465.8	2335.3	4981.5
4/25/2012	B1	Coliforms	49	26	25	1953.8	1240.2	2885.8
4/25/2012	B2	Coliforms	49	23	25	1642.3	1042.5	2475.7
4/25/2012	B3	Coliforms	49	18	25	1230.4	781	1884.9
4/25/2012	DPin	<i>E. coli</i>	44	12	25	533.8	380.5	711.6
4/25/2012	DPout	<i>E. coli</i>	11	1	25	53.4	29.8	89.2
4/25/2012	B1	<i>E. coli</i>	19	4	25	113.9	72.3	167.2
4/25/2012	B2	<i>E. coli</i>	20	1	25	104.8	66.6	158.8
4/25/2012	B3	<i>E. coli</i>	12	0	25	54	31.1	93.6
4/25/2012	DPin	Enterococci	49	21	100	365.4	231.9	555.5
4/25/2012	DPout	Enterococci	12	2	100	15.8	8.8	25.7

4/25/2012	B1	Enterococci	19	8	100	33.7	22.7	48
4/25/2012	B2	Enterococci	6	1	100	7.4	3.2	14.4
4/25/2012	B3	Enterococci	7	1	100	8.5	3.9	15.6
5/3/2012	DPin	Coliforms	49	39	10	10462.4	7049.9	15090.3
5/3/2012	DPout	Coliforms	49	30	10	6131.4	4011.8	8792.1
5/3/2012	B1	Coliforms	49	13	10	2359.3	1589.7	3600
5/3/2012	B2	Coliforms	48	20	10	2723	1834.9	3828.9
5/3/2012	B3	Coliforms	48	14	10	2098.2	1454.8	3011.1
5/3/2012	DPin	<i>E. coli</i>	33	9	10	675.6	494.8	915.9
5/3/2012	DPout	<i>E. coli</i>	6	0	10	63.2	29	137.1
5/3/2012	B1	<i>E. coli</i>	17	1	10	215.7	128.5	337.1
5/3/2012	B2	<i>E. coli</i>	25	1	10	349.8	228.8	511.8
5/3/2012	B3	<i>E. coli</i>	10	2	10	132.3	71	220.1
5/3/2012	DPin	Enterococci	43	17	100	143	107.5	187.2
5/3/2012	DPout	Enterococci	2	3	100	5.1	1.6	10.6
5/3/2012	B1	Enterococci	18	5	100	28.1	18.4	41.3
5/3/2012	B2	Enterococci	13	3	100	18.3	10.5	28.8
5/3/2012	B3	Enterococci	5	3	100	8.4	3.7	15.3
5/10/2012	DPin	Coliforms	49	47	10	24195.7	16303.7	47161
5/10/2012	DPout	Coliforms	49	40	10	11198.7	7546	16140
5/10/2012	B1	Coliforms	49	27	10	5172.1	3384.1	7635.6
5/10/2012	B2	Coliforms	49	28	10	5475	3582.3	8044.5
5/10/2012	B3	Coliforms	49	46	10	19862.9	12220.3	33002.3
5/10/2012	DPin	<i>E. coli</i>	23	5	10	368.4	248.3	522.1
5/10/2012	DPout	<i>E. coli</i>	20	6	10	327.7	220.8	471.7
5/10/2012	B1	<i>E. coli</i>	16	4	10	237.8	146.3	357.7
5/10/2012	B2	<i>E. coli</i>	33	0	10	512.2	345.2	722.9
5/10/2012	B3	<i>E. coli</i>	49	45	10	17328.9	11676.7	27094.7
5/10/2012	DPin	Enterococci	43	22	100	163.8	123.1	212.3
5/10/2012	DPout	Enterococci	17	7	100	29.1	19	42
5/10/2012	B1	Enterococci	24	8	100	43.1	29.9	59.8
5/10/2012	B2	Enterococci	31	14	100	70.5	51.7	93.9
5/10/2012	B3	Enterococci	49	47	100	2419.6	1630.4	4716.1
5/16/2012	DPin	Coliforms	49	45	10	17328.9	11676.7	27094.7
5/16/2012	DPout	Coliforms	49	44	10	15531.2	10162	23530.6
5/16/2012	B1	Coliforms	49	25	10	4611.1	2927	6878.8
5/16/2012	B2	Coliforms	49	31	10	6488.2	4245.2	9414.6
5/16/2012	B3	Coliforms	49	30	10	6131.4	4011.8	8792.1
5/16/2012	DPin	<i>E. coli</i>	28	5	10	472.5	327.6	658.8
5/16/2012	DPout	<i>E. coli</i>	28	3	10	441.2	305.9	625.2
5/16/2012	B1	<i>E. coli</i>	23	3	10	340.5	222.8	491.9
5/16/2012	B2	<i>E. coli</i>	30	4	10	503.9	349.4	700.8
5/16/2012	B3	<i>E. coli</i>	27	1	10	389.3	262.4	558.9
5/16/2012	DPin	Enterococci	48	27	100	378.4	262.4	526.2
5/16/2012	DPout	Enterococci	46	10	100	146.7	104.6	201.1
5/16/2012	B1	Enterococci	38	11	100	91	66.6	121
5/16/2012	B2	Enterococci	37	10	100	84.2	61.7	112.2
5/16/2012	B3	Enterococci	43	17	100	143	107.5	187.2
5/23/2012	DPin	Coliforms	49	43	10	14136.1	9249.2	21016.2
5/23/2012	DPout	Coliforms	49	25	10	4611.1	2927	6878.8
5/23/2012	B1	Coliforms	49	26	10	4884.4	3100.4	7214.5
5/23/2012	B2	Coliforms	47	26	10	2924	2141.6	3883.8
5/23/2012	B3	Coliforms	48	20	10	2723	1834.9	3828.9
5/23/2012	DPin	<i>E. coli</i>	41	11	10	1071.2	784.6	1426.6

5/23/2012	DPout	<i>E. coli</i>	18	1	10	230.7	141.9	356.9
5/23/2012	B1	<i>E. coli</i>	15	1	10	186.9	107.7	299.8
5/23/2012	B2	<i>E. coli</i>	22	0	10	282	179	422.5
5/23/2012	B3	<i>E. coli</i>	19	1	10	246.2	151.4	376.4
5/23/2012	DPin	Enterococci	49	14	100	248.1	162.3	371.9
5/23/2012	DPout	Enterococci	33	11	100	71.4	52.3	94.6
5/23/2012	B1	Enterococci	37	6	100	75.4	53.8	102.6
5/23/2012	B2	Enterococci	34	5	100	63.1	45	86.9
5/23/2012	B3	Enterococci	28	2	100	42.6	28.7	60.7
5/30/2012	DPin	Coliforms	49	46	10	19862.9	12220.3	33002.3
5/30/2012	DPout	Coliforms	49	47	10	24195.7	16303.7	47161
5/30/2012	B1	Coliforms	49	44	10	15531.2	10162	23530.6
5/30/2012	B2	Coliforms	49	42	10	12996.5	8503.6	18965.6
5/30/2012	B3	Coliforms	49	41	10	12033.3	8108.4	17507
5/30/2012	DPin	<i>E. coli</i>	48	20	10	2723	1834.9	3828.9
5/30/2012	DPout	<i>E. coli</i>	46	17	10	1841.8	1349	2513.7
5/30/2012	B1	<i>E. coli</i>	26	5	10	428.4	297	600.8
5/30/2012	B2	<i>E. coli</i>	39	8	10	884.1	630.3	1191.7
5/30/2012	B3	<i>E. coli</i>	26	8	10	473.7	328.4	654.2
5/30/2012	DPin	Enterococci	49	43	100	1413.6	924.9	2101.6
5/30/2012	DPout	Enterococci	49	42	100	1299.7	850.4	1896.6
5/30/2012	B1	Enterococci	49	26	100	488.4	310	721.5
5/30/2012	B2	Enterococci	49	30	100	613.1	401.2	879.2
5/30/2012	B3	Enterococci	49	27	100	517.2	338.4	763.6
6/4/2012	DPin	Coliforms	49	42	10	12996.5	8503.6	18965.6
6/4/2012	DPout	Coliforms	49	47	10	24195.7	16303.7	47161
6/4/2012	B1	Coliforms	49	27	10	5172.1	3384.1	7635.6
6/4/2012	B2	Coliforms	49	30	10	6131.4	4011.8	8792.1
6/4/2012	B3	Coliforms	48	29	10	4160.2	2965.8	5566.7
6/4/2012	DPin	<i>E. coli</i>	27	2	10	404.4	272.5	574.1
6/4/2012	DPout	<i>E. coli</i>	6	2	10	84.4	37.1	153.4
6/4/2012	B1	<i>E. coli</i>	13	1	10	159.6	91.9	263.7
6/4/2012	B2	<i>E. coli</i>	17	1	10	215.7	128.5	337.1
6/4/2012	B3	<i>E. coli</i>	19	1	10	246.2	151.4	376.4
6/4/2012	DPin	Enterococci	49	35	100	816.4	550.1	1174.6
6/4/2012	DPout	Enterococci	27	2	100	40.4	27.3	57.4
6/4/2012	B1	Enterococci	44	11	100	129.6	95	174.4
6/4/2012	B2	Enterococci	48	11	100	186	125.3	268.8
6/4/2012	B3	Enterococci	45	8	100	127.4	90.8	176.4
6/11/2012	DPin	Coliforms	49	39	10	10462.4	7049.9	15090.3
6/11/2012	DPout	Coliforms	49	21	10	3654	2319.4	5554.5
6/11/2012	B1	Coliforms	49	19	10	3255.4	2066.4	4980.8
6/11/2012	B2	Coliforms	48	22	10	2986.6	2070.8	4231.7
6/11/2012	B3	Coliforms	48	20	10	2723	1834.9	3828.9
6/11/2012	DPin	<i>E. coli</i>	38	7	10	816.2	581.9	1103.2
6/11/2012	DPout	<i>E. coli</i>	14	3	10	196.7	117.2	306.9
6/11/2012	B1	<i>E. coli</i>	32	3	10	538.1	373.1	750.4
6/11/2012	B2	<i>E. coli</i>	18	3	10	255.9	157.4	383.6
6/11/2012	B3	<i>E. coli</i>	20	3	10	288.2	182.9	427.1
6/11/2012	DPin	Enterococci	49	25	100	461.1	292.7	687.9
6/11/2012	DPout	Enterococci	45	17	100	167.4	122.6	222.7
6/11/2012	B1	Enterococci	49	30	100	613.1	401.2	879.2
6/11/2012	B2	Enterococci	39	15	100	106.3	77.9	138.7
6/11/2012	B3	Enterococci	26	6	100	44.3	30.7	61.8

6/18/2012	DPin	Coliforms	49	46	2	99314.5	61101.5	165011.5
6/18/2012	DPout	Coliforms	49	47	5	48391.4	32607.4	94322
6/18/2012	B1	Coliforms	49	40	5	22397.4	15092	32280
6/18/2012	B2	Coliforms	49	44	5	31062.4	20324	47061.2
6/18/2012	B3	Coliforms	49	43	5	28272.2	18498.4	42032.4
6/18/2012	DPin	<i>E. coli</i>	39	7	2	4300	3065.5	5775.5
6/18/2012	DPout	<i>E. coli</i>	43	11	5	2422.4	1774.2	3265.2
6/18/2012	B1	<i>E. coli</i>	44	12	5	2668.8	1902.6	3558.2
6/18/2012	B2	<i>E. coli</i>	41	9	5	2028.8	1486	2722
6/18/2012	B3	<i>E. coli</i>	39	11	5	1917.2	1404.2	2551.2
6/18/2012	DPin	Enterococci	49	30	50	1226.3	802.4	1758.4
6/18/2012	DPout	Enterococci	49	47	100	2419.6	1630.4	4716.1
6/18/2012	B1	Enterococci	49	44	100	1553.1	1016.2	2353.1
6/18/2012	B2	Enterococci	49	46	100	1986.3	1222	3300.2
6/18/2012	B3	Enterococci	49	44	100	1553.1	1016.2	2353.1
6/25/2012	DPin	Coliforms	48	20	5	5446	3669.8	7657.8
6/25/2012	DPout	Coliforms	49	32	5	13733.4	8985.8	19488.2
6/25/2012	B1	Coliforms	49	20	5	6896	4377.4	10413.2
6/25/2012	B2	Coliforms	49	16	5	5510.2	3713	8335.2
6/25/2012	B3	Coliforms	49	16	5	5510.2	3713	8335.2
6/25/2012	DPin	<i>E. coli</i>	16	1	5	402.2	247.4	636.8
6/25/2012	DPout	<i>E. coli</i>	6	0	5	126.4	58	274.2
6/25/2012	B1	<i>E. coli</i>	15	1	5	373.8	215.4	599.6
6/25/2012	B2	<i>E. coli</i>	13	0	5	296	170.6	501.2
6/25/2012	B3	<i>E. coli</i>	12	2	5	315.8	175.8	514.2
6/25/2012	DPin	Enterococci	19	4	50	56.9	36.1	83.6
6/25/2012	DPout	Enterococci	47	15	100	191.8	136.7	264.5
6/25/2012	B1	Enterococci	42	13	100	120.1	87.9	159.8
6/25/2012	B2	Enterococci	43	10	100	117.8	86.3	158.2
6/25/2012	B3	Enterococci	36	6	100	71.7	51.1	97.5
7/2/2012	DPin	Coliforms	49	42	1	129965	85036	189656
7/2/2012	DPout	Coliforms	49	47	1	241957	163037	471610
7/2/2012	B1	Coliforms	49	46	1	198629	122203	330023
7/2/2012	B2	Coliforms	49	44	1	155312	101620	235306
7/2/2012	B3	Coliforms	49	42	1	129965	85036	189656
7/2/2012	DPin	<i>E. coli</i>	40	10	2	4927	3608.5	6607
7/2/2012	DPout	<i>E. coli</i>	49	43	5	28272.2	18498.4	42032.4
7/2/2012	B1	<i>E. coli</i>	49	26	5	9768.8	6200.8	14429
7/2/2012	B2	<i>E. coli</i>	49	21	5	7308	4638.8	11109
7/2/2012	B3	<i>E. coli</i>	49	17	5	5818.6	3807.2	8921
7/2/2012	DPin	Enterococci	49	46	50	3972.6	2444.1	6600.5
7/2/2012	DPout	Enterococci	49	47	100	2419.6	1630.4	4716.1
7/2/2012	B1	Enterococci	49	46	100	1986.3	1222	3300.2
7/2/2012	B2	Enterococci	49	46	100	1986.3	1222	3300.2
7/2/2012	B3	Enterococci	49	36	100	866.4	583.8	1245.4
7/9/2012	DPin	Coliforms	49	17	2	14546.5	9518	22302.5
7/9/2012	DPout	Coliforms	49	18	2	15379.5	9762.5	23561.5
7/9/2012	B1	Coliforms	49	32	2	34333.5	22464.5	48720.5
7/9/2012	B2	Coliforms	49	23	2	20529	13031	30946
7/9/2012	B3	Coliforms	44	10	2	6295.5	4611	8598
7/9/2012	DPin	<i>E. coli</i>	15	3	2	1054.5	628	1628
7/9/2012	DPout	<i>E. coli</i>	0	1	2	49.5	1.5	183.5
7/9/2012	B1	<i>E. coli</i>	23	1	2	1564.5	1023.5	2299.5
7/9/2012	B2	<i>E. coli</i>	16	0	2	945	563	1518

7/9/2012	B3	<i>E. coli</i>	4	2	2	310	118	612
7/9/2012	DPin	Enterococci	37	9	50	163.9	120.1	218.8
7/9/2012	DPout	Enterococci	7	2	50	19.2	8.8	33.9
7/9/2012	B1	Enterococci	46	34	50	662.8	511.3	846
7/9/2012	B2	Enterococci	47	31	50	715.5	524.1	942.5
7/9/2012	B3	Enterococci	11	2	50	29	15.6	47.1
7/16/2012	DPin	Coliforms	49	45	3	57763	38922.3	90315.7
7/16/2012	DPout	Coliforms	49	17	3	9697.7	6345.3	14868.3
7/16/2012	B1	Coliforms	49	16	3	9183.7	6188.3	13892
7/16/2012	B2	Coliforms	43	9	3	3815.3	2720	5182.7
7/16/2012	B3	Coliforms	43	16	3	4638	3397	6067.7
7/16/2012	DPin	<i>E. coli</i>	28	1	3	1367.7	921.7	1959.7
7/16/2012	DPout	<i>E. coli</i>	2	0	3	67.3	8.7	237.7
7/16/2012	B1	<i>E. coli</i>	10	2	3	441	236.7	733.7
7/16/2012	B2	<i>E. coli</i>	4	0	3	137.7	55	317.3
7/16/2012	B3	<i>E. coli</i>	4	0	3	137.7	55	317.3
7/16/2012	DPin	Enterococci	49	32	50	1373.3	898.6	1948.8
7/16/2012	DPout	Enterococci	12	1	50	29.3	16.3	49.2
7/16/2012	B1	Enterococci	28	9	50	107.2	76.4	146
7/16/2012	B2	Enterococci	13	5	50	41.3	25.4	63.7
7/16/2012	B3	Enterococci	14	2	50	37	22	58.4
7/23/2012	DPin	Coliforms	49	41	3	40111	27028	58356.7
7/23/2012	DPout	Coliforms	49	38	3	32679.7	22020.3	47005.3
7/23/2012	B1	Coliforms	49	38	3	32679.7	22020.3	47005.3
7/23/2012	B2	Coliforms	49	21	3	12180	7731.3	18515
7/23/2012	B3	Coliforms	49	19	3	10851.3	6888	16602.7
7/23/2012	DPin	<i>E. coli</i>	6	0	3	210.7	96.7	457
7/23/2012	DPout	<i>E. coli</i>	7	0	3	248.3	118.7	495.7
7/23/2012	B1	<i>E. coli</i>	42	0	3	2753.3	1909	3845
7/23/2012	B2	<i>E. coli</i>	4	1	3	172	58.7	358.7
7/23/2012	B3	<i>E. coli</i>	5	0	3	173.7	76.3	398
7/23/2012	DPin	Enterococci	19	3	50	54.4	34.5	80.4
7/23/2012	DPout	Enterococci	32	7	50	121.7	86.8	166.5
7/23/2012	B1	Enterococci	39	10	50	186.7	136.7	248.4
7/23/2012	B2	Enterococci	31	8	50	119.6	85.3	162.7
7/23/2012	B3	Enterococci	23	5	50	73.7	49.7	104.4
7/30/2012	DPin	Coliforms	49	29	3	19314.3	12637.3	28239
7/30/2012	DPout	Coliforms	49	32	3	22889	14976.3	32480.3
7/30/2012	B1	Coliforms	46	9	3	4736.3	3376.7	6561
7/30/2012	B2	Coliforms	46	14	3	5565	3967	7596
7/30/2012	B3	Coliforms	44	5	3	3620	2580.7	4999.7
7/30/2012	DPin	<i>E. coli</i>	1	0	3	33.3	1.7	183
7/30/2012	DPout	<i>E. coli</i>	6	0	3	210.7	96.7	457
7/30/2012	B1	<i>E. coli</i>	6	1	3	246	108	480
7/30/2012	B2	<i>E. coli</i>	3	1	3	136.3	38.7	302.3
7/30/2012	B3	<i>E. coli</i>	1	0	3	33.3	1.7	183
7/30/2012	DPin	Enterococci	7	2	50	19.2	8.8	33.9
7/30/2012	DPout	Enterococci	29	3	50	92.8	62.5	130.7
7/30/2012	B1	Enterococci	23	3	50	68.1	44.6	98.4
7/30/2012	B2	Enterococci	21	4	50	63.7	41.7	92.7
7/30/2012	B3	Enterococci	22	1	50	59.1	37.5	87.9
8/7/2012	DPin	Coliforms	49	36	3	28881.3	19461	41512.7
8/7/2012	DPout	Coliforms	49	23	3	13686	8687.3	20630.7
8/7/2012	B1	Coliforms	46	9	3	4736.3	3376.7	6561

8/7/2012	B2	Coliforms	47	12	3	5744.3	3983	8074
8/7/2012	B3	Coliforms	48	8	3	5525.3	3831	7931.7
8/7/2012	DPin	<i>E. coli</i>	13	3	3	609.7	351.3	960.7
8/7/2012	DPout	<i>E. coli</i>	9	0	3	326.3	156	612
8/7/2012	B1	<i>E. coli</i>	3	0	3	102	23	298
8/7/2012	B2	<i>E. coli</i>	3	0	3	102	23	298
8/7/2012	B3	<i>E. coli</i>	2	1	3	101.3	22.7	245.7
8/7/2012	DPin	Enterococci	8	0	50	17.2	8.9	33.7
8/7/2012	DPout	Enterococci	21	0	50	53.1	33.7	80.2
8/7/2012	B1	Enterococci	16	2	50	42.7	25.4	65.2
8/7/2012	B2	Enterococci	16	1	50	40.2	24.7	63.7
8/7/2012	B3	Enterococci	7	2	50	19.2	8.8	33.9
8/13/2012	DPin	Coliforms	49	17	3	9697.7	6345.3	14868.3
8/13/2012	DPout	Coliforms	49	30	3	20438	13372.7	29307
8/13/2012	B1	Coliforms	48	14	3	6994	4849.3	10037
8/13/2012	B2	Coliforms	48	8	3	5525.3	3831	7931.7
8/13/2012	B3	Coliforms	47	10	3	5357	3714.3	7545
8/13/2012	DPin	<i>E. coli</i>	8	1	3	323	148.3	572
8/13/2012	DPout	<i>E. coli</i>	8	0	3	286.7	148.3	562.3
8/13/2012	B1	<i>E. coli</i>	8	1	3	323	148.3	572
8/13/2012	B2	<i>E. coli</i>	4	0	3	137.7	55	317.3
8/13/2012	B3	<i>E. coli</i>	1	1	3	67	8.3	197.3
8/13/2012	DPin	Enterococci	10	2	50	26.5	14.2	44
8/13/2012	DPout	Enterococci	44	9	50	244.6	174.4	334.5
8/13/2012	B1	Enterococci	22	2	50	61.8	39.2	90.9
8/13/2012	B2	Enterococci	14	1	50	34.6	20.6	56.3
8/13/2012	B3	Enterococci	9	1	50	21.8	11.3	39
8/20/2012	DPin	Coliforms	49	39	3	34874.7	23499.7	50301
8/20/2012	DPout	Coliforms	49	45	3	57763	38922.3	90315.7
8/20/2012	B1	Coliforms	49	27	3	17240.3	11280.3	25452
8/20/2012	B2	Coliforms	49	22	3	12910.7	8195.3	18901.3
8/20/2012	B3	Coliforms	49	16	3	9183.7	6188.3	13892
8/20/2012	DPin	<i>E. coli</i>	24	1	3	1103.3	722	1604.3
8/20/2012	DPout	<i>E. coli</i>	44	5	3	3620	2580.7	4999.7
8/20/2012	B1	<i>E. coli</i>	11	0	3	407.7	227	713.3
8/20/2012	B2	<i>E. coli</i>	9	2	3	399.7	199	675.7
8/20/2012	B3	<i>E. coli</i>	3	1	3	136.3	38.7	302.3
8/20/2012	DPin	Enterococci	49	41	100	1203.3	810.8	1750.7
8/20/2012	DPout	Enterococci	49	47	100	2419.6	1630.4	4716.1
8/20/2012	B1	Enterococci	48	15	100	218.7	151.7	314.5
8/20/2012	B2	Enterococci	43	12	100	124.6	91.2	167.8
8/20/2012	B3	Enterococci	42	13	100	120.1	87.9	159.8
8/27/2012	DPin	Coliforms	49	31	3	21627.3	14150.7	31382
8/27/2012	DPout	Coliforms	47	9	3	5175	3588.3	7290.7
8/27/2012	B1	Coliforms	47	7	3	4832.3	3350.7	6825.3
8/27/2012	B2	Coliforms	45	10	3	4513.3	3217.7	6133.7
8/27/2012	B3	Coliforms	42	5	3	3199.7	2281	4389.3
8/27/2012	DPin	<i>E. coli</i>	9	1	3	363	187.7	649.7
8/27/2012	DPout	<i>E. coli</i>	2	1	3	101.3	22.7	245.7
8/27/2012	B1	<i>E. coli</i>	10	1	3	403.7	216.7	703
8/27/2012	B2	<i>E. coli</i>	3	1	3	136.3	38.7	302.3
8/27/2012	B3	<i>E. coli</i>	8	1	3	323	148.3	572
8/27/2012	DPin	Enterococci	39	22	100	126.1	94.9	160.7
8/27/2012	DPout	Enterococci	17	3	100	24.1	14.8	36.5

8/27/2012	B1	Enterococci	41	14	100	116	87.2	152.6
8/27/2012	B2	Enterococci	15	2	100	19.9	11.9	30.9
8/27/2012	B3	Enterococci	20	6	100	32.8	22.1	47.2
9/3/2012	DPin	Coliforms	49	47	3	80652.3	54345.7	157203.3
9/3/2012	DPout	Coliforms	49	30	3	20438	13372.7	29307
9/3/2012	B1	Coliforms	49	27	3	17240.3	11280.3	25452
9/3/2012	B2	Coliforms	49	23	3	13686	8687.3	20630.7
9/3/2012	B3	Coliforms	49	25	3	15370.3	9756.7	22929.3
9/3/2012	DPin	<i>E. coli</i>	33	5	3	2005	1429.3	2765.7
9/3/2012	DPout	<i>E. coli</i>	27	1	3	1297.7	874.7	1863
9/3/2012	B1	<i>E. coli</i>	13	2	3	570.7	329	913
9/3/2012	B2	<i>E. coli</i>	13	1	3	532	306.3	879
9/3/2012	B3	<i>E. coli</i>	10	1	3	403.7	216.7	703
9/3/2012	DPin	Enterococci	33	34	100	120.5	95.3	148.2
9/3/2012	DPout	Enterococci	33	17	100	83.2	62.6	108.3
9/3/2012	B1	Enterococci	44	30	100	223.5	172.4	282.2
9/3/2012	B2	Enterococci	42	28	100	177.3	136.8	222.7
9/3/2012	B3	Enterococci	41	18	100	128.7	94.2	168
9/10/2012	DPin	Coliforms	49	33	3	24233	15855.7	34962.3
9/10/2012	DPout	Coliforms	48	18	3	8296.7	5752.7	11674.7
9/10/2012	B1	Coliforms	48	19	3	8675	5845.3	12173
9/10/2012	B2	Coliforms	48	11	3	6200	4177.7	8958.7
9/10/2012	B3	Coliforms	49	17	3	9697.7	6345.3	14868.3
9/10/2012	DPin	<i>E. coli</i>	2	2	3	135	38.3	298.3
9/10/2012	DPout	<i>E. coli</i>	6	1	3	246	108	480
9/10/2012	B1	<i>E. coli</i>	29	5	3	1653	1146	2282.7
9/10/2012	B2	<i>E. coli</i>	40	5	3	2858	2037.7	3906
9/10/2012	B3	<i>E. coli</i>	30	5	3	1734.7	1202.7	2407
9/10/2012	DPin	Enterococci	49	19	100	325.5	206.6	498.1
9/10/2012	DPout	Enterococci	49	38	100	980.4	660.6	1410.2
9/10/2012	B1	Enterococci	49	27	100	517.2	338.4	763.6
9/10/2012	B2	Enterococci	48	21	100	285.1	197.7	398.8
9/10/2012	B3	Enterococci	46	16	100	178.2	130.5	243.1
9/17/2012	DPin	Coliforms	49	46	3	66209.7	40734.3	110007.7
9/17/2012	DPout	Coliforms	48	11	3	6200	4177.7	8958.7
9/17/2012	B1	Coliforms	49	39	3	34874.7	23499.7	50301
9/17/2012	B2	Coliforms	49	20	3	11493.3	7295.7	17355.3
9/17/2012	B3	Coliforms	48	9	3	5738.7	3979	8165.3
9/17/2012	DPin	<i>E. coli</i>	27	3	3	1398.3	942.3	1990
9/17/2012	DPout	<i>E. coli</i>	11	1	3	445.3	248	743.7
9/17/2012	B1	<i>E. coli</i>	49	20	3	11493.3	7295.7	17355.3
9/17/2012	B2	<i>E. coli</i>	45	12	3	4795.7	3419	6500
9/17/2012	B3	<i>E. coli</i>	42	3	3	3016.3	2091.7	4165.7
9/17/2012	DPin	Enterococci	49	41	50	2406.7	1621.7	3501.4
9/17/2012	DPout	Enterococci	46	11	100	151.5	108	207.8
9/17/2012	B1	Enterococci	48	37	50	1203	881.1	1608.9
9/17/2012	B2	Enterococci	49	44	100	1553.1	1016.2	2353.1
9/17/2012	B3	Enterococci	49	41	100	1203.3	810.8	1750.7
9/22/2012	DPin	Coliforms	49	41	3	40111	27028	58356.7
9/22/2012	DPout	Coliforms	47	19	3	7412	5284	10108.3
9/22/2012	B1	Coliforms	45	12	3	4795.7	3419	6500
9/22/2012	B2	Coliforms	46	5	3	4166	2888.7	5894.7
9/22/2012	B3	Coliforms	45	4	3	3754.7	2603.3	5218.3
9/22/2012	DPin	<i>E. coli</i>	48	21	3	9503.3	6589.3	13292

9/22/2012	DPout	<i>E. coli</i>	8	1	3	323	148.3	572
9/22/2012	B1	<i>E. coli</i>	4	0	3	137.7	55	317.3
9/22/2012	B2	<i>E. coli</i>	5	0	3	173.7	76.3	398
9/22/2012	B3	<i>E. coli</i>	7	0	3	248.3	118.7	495.7
9/22/2012	DPin	Enterococci	21	3	50	61	38.7	89.5
9/22/2012	DPout	Enterococci	7	4	50	23.5	12.2	40.2
9/22/2012	B1	Enterococci	31	2	50	99.1	68.7	138.6
9/22/2012	B2	Enterococci	26	7	50	91.7	63.6	127
9/22/2012	B3	Enterococci	34	5	50	126.3	90	173.9
10/3/2012	DPin	Coliforms	49	35	3	27213.7	18337.3	39153
10/3/2012	DPout	Coliforms	48	14	3	6994	4849.3	10037
10/3/2012	B1	Coliforms	38	7	3	2720.7	1939.7	3677.3
10/3/2012	B2	Coliforms	39	7	3	2866.7	2043.7	3850.3
10/3/2012	B3	Coliforms	37	3	3	2302.3	1596.3	3185.3
10/3/2012	DPin	<i>E. coli</i>	36	7	3	2460	1753.7	3317.3
10/3/2012	DPout	<i>E. coli</i>	13	1	3	532	306.3	879
10/3/2012	B1	<i>E. coli</i>	6	0	3	210.7	96.7	457
10/3/2012	B2	<i>E. coli</i>	2	1	3	101.3	22.7	245.7
10/3/2012	B3	<i>E. coli</i>	5	0	3	173.7	76.3	398
10/3/2012	DPin	Enterococci	49	42	50	2599.3	1700.7	3793.1
10/3/2012	DPout	Enterococci	38	6	50	158.7	113.1	215.4
10/3/2012	B1	Enterococci	36	5	50	139.4	99.4	190.5
10/3/2012	B2	Enterococci	29	6	50	102.4	71	141.4
10/3/2012	B3	Enterococci	27	6	50	93.1	64.5	129.5
10/8/2012	DPin	Coliforms	49	22	3	12910.7	8195.3	18901.3
10/8/2012	DPout	Coliforms	41	9	3	3381.3	2476.7	4536.7
10/8/2012	B1	Coliforms	49	35	3	27213.7	18337.3	39153
10/8/2012	B2	Coliforms	40	8	3	3110.3	2217.3	4180.7
10/8/2012	B3	Coliforms	41	6	3	3108.7	2216.3	4211.3
10/8/2012	DPin	<i>E. coli</i>	34	1	3	1857.7	1288	2595.3
10/8/2012	DPout	<i>E. coli</i>	12	1	3	488	271.7	820.7
10/8/2012	B1	<i>E. coli</i>	49	35	3	27213.7	18337.3	39153
10/8/2012	B2	<i>E. coli</i>	5	3	3	278.7	122.3	509.7
10/8/2012	B3	<i>E. coli</i>	7	1	3	284	130.3	521.3
10/8/2012	DPin	Enterococci	46	2	50	226.9	157.3	319.8
10/8/2012	DPout	Enterococci	42	0	50	165.2	114.5	230.7
10/8/2012	B1	Enterococci	39	7	50	172	122.6	231
10/8/2012	B2	Enterococci	32	5	50	114.6	79.5	158.2
10/8/2012	B3	Enterococci	29	7	50	105.7	73.3	144.6
10/15/2012	DPin	Coliforms	49	47	3	80652.3	54345.7	157203.3
10/15/2012	DPout	Coliforms	48	20	3	9076.7	6116.3	12763
10/15/2012	B1	Coliforms	49	11	3	7142	4673	10698
10/15/2012	B2	Coliforms	46	13	3	5387.3	3840.7	7351.7
10/15/2012	B3	Coliforms	47	16	3	6630	4726.3	9111.3
10/15/2012	DPin	<i>E. coli</i>	47	14	3	6167	4396.3	8541.7
10/15/2012	DPout	<i>E. coli</i>	22	1	3	984.7	625	1465.7
10/15/2012	B1	<i>E. coli</i>	14	3	3	655.7	390.7	1023
10/15/2012	B2	<i>E. coli</i>	12	2	3	526.3	293	857
10/15/2012	B3	<i>E. coli</i>	18	2	3	811	514.7	1235.3
10/15/2012	DPin	Enterococci	28	3	50	88.2	61.2	125
10/15/2012	DPout	Enterococci	15	1	50	37.4	21.5	60
10/15/2012	B1	Enterococci	18	2	50	48.7	30.9	74.1
10/15/2012	B2	Enterococci	29	7	50	105.7	73.3	144.6
10/15/2012	B3	Enterococci	35	10	50	152.7	111.8	202.3

10/22/2012	DPin	Coliforms	49	46	3	66209.7	40734.3	110007.7
10/22/2012	DPout	Coliforms	37	6	3	2513.7	1792	3419.3
10/22/2012	B1	Coliforms	20	2	3	917	582	1372.7
10/22/2012	B2	Coliforms	17	3	3	801.7	493.3	1215
10/22/2012	B3	Coliforms	25	2	3	1213.7	794	1751.7
10/22/2012	DPin	<i>E. coli</i>	38	13	3	3194.3	2339.7	4201
10/22/2012	DPout	<i>E. coli</i>	1	1	3	67	8.3	197.3
10/22/2012	B1	<i>E. coli</i>	2	1	3	101.3	22.7	245.7
10/22/2012	B2	<i>E. coli</i>	7	0	3	248.3	118.7	495.7
10/22/2012	B3	<i>E. coli</i>	5	2	3	243.7	97.7	463
10/22/2012	DPin	Enterococci	14	0	50	32.3	18.6	53.6
10/22/2012	DPout	Enterococci	8	2	50	21.6	10.3	37.2
10/22/2012	B1	Enterococci	9	2	50	24	11.9	40.5
10/22/2012	B2	Enterococci	11	0	50	24.5	13.6	42.8
10/22/2012	B3	Enterococci	13	2	50	34.2	19.7	54.8
10/29/2012	DPin	Coliforms	49	44	5	31062.4	20324	47061.2
10/29/2012	DPout	Coliforms	44	10	5	2518.2	1844.4	3439.2
10/29/2012	B1	Coliforms	49	31	5	12976.4	8490.4	18829.2
10/29/2012	B2	Coliforms	49	33	5	14539.8	9513.4	20977.4
10/29/2012	B3	Coliforms	49	30	5	12262.8	8023.6	17584.2
10/29/2012	DPin	<i>E. coli</i>	36	6	5	1434.6	1022.8	1949.2
10/29/2012	DPout	<i>E. coli</i>	4	0	5	82.6	33	190.4
10/29/2012	B1	<i>E. coli</i>	49	15	5	5225	3418.8	7969
10/29/2012	B2	<i>E. coli</i>	49	16	5	5510.2	3713	8335.2
10/29/2012	B3	<i>E. coli</i>	48	11	5	3720	2506.6	5375.2
10/29/2012	DPin	Enterococci	23	24	50	129.5	97.4	166.5
10/29/2012	DPout	Enterococci	12	3	50	33.9	18.9	54.1
10/29/2012	B1	Enterococci	36	25	50	230.5	177.8	290.8
10/29/2012	B2	Enterococci	42	43	50	514.9	417.4	621.8
10/29/2012	B3	Enterococci	47	44	50	1187.6	916.2	1527.1
11/5/2012	DPin	Coliforms	49	45	5	34657.8	23353.4	54189.4
11/5/2012	DPout	Coliforms	49	28	5	10950	7164.6	16089
11/5/2012	B1	Coliforms	35	4	5	1287.4	892.6	1772.2
11/5/2012	B2	Coliforms	33	2	5	1095	759.2	1528.2
11/5/2012	B3	Coliforms	31	4	5	1058.2	733.6	1473.2
11/5/2012	DPin	<i>E. coli</i>	45	11	5	2791.6	1990	3799.2
11/5/2012	DPout	<i>E. coli</i>	22	5	5	699.6	471.4	1006.8
11/5/2012	B1	<i>E. coli</i>	4	0	5	82.6	33	190.4
11/5/2012	B2	<i>E. coli</i>	12	0	5	270	155.6	468
11/5/2012	B3	<i>E. coli</i>	9	0	5	195.8	93.6	367.2
11/5/2012	DPin	Enterococci	47	48	50	1382.1	1093.2	1773.1
11/5/2012	DPout	Enterococci	33	14	50	154.4	116.1	202
11/5/2012	B1	Enterococci	6	3	50	19	8.7	33.9
11/5/2012	B2	Enterococci	6	5	50	23.3	12.1	40.2
11/5/2012	B3	Enterococci	7	1	50	17	7.8	31.3
11/12/2012	DPin	Coliforms	49	34	5	15402	10980	21880.6
11/12/2012	DPout	Coliforms	12	1	5	292.8	163	492.4
11/12/2012	B1	Coliforms	11	2	5	289.8	155.8	471.4
11/12/2012	B2	Coliforms	18	1	5	461.4	283.8	713.8
11/12/2012	B3	Coliforms	16	0	5	378	225.2	607.2
11/12/2012	DPin	<i>E. coli</i>	29	2	5	895.8	603.6	1267.2
11/12/2012	DPout	<i>E. coli</i>	1	0	5	20	1	109.8
11/12/2012	B1	<i>E. coli</i>	3	1	5	81.8	23.2	181.4
11/12/2012	B2	<i>E. coli</i>	3	0	5	61.2	13.8	178.8

11/12/2012	B3	<i>E. coli</i>	7	0	5	149	71.2	297.4
11/12/2012	DPin	Enterococci	49	24	50	870.3	552.5	1300.1
11/12/2012	DPout	Enterococci	11	0	50	24.5	13.6	42.8
11/12/2012	B1	Enterococci	20	1	100	26.2	16.6	39.7
11/12/2012	B2	Enterococci	20	0	100	24.9	15.8	38.1
11/12/2012	B3	Enterococci	28	0	100	39.5	25.9	57
11/18/2012	DPin	Coliforms	49	43	10	14136.1	9249.2	21016.2
11/18/2012	DPout	Coliforms	42	7	10	1016.8	724.8	1382.4
11/18/2012	B1	Coliforms	30	3	10	487.4	338	680.2
11/18/2012	B2	Coliforms	23	1	10	312.9	204.7	459.9
11/18/2012	B3	Coliforms	17	2	10	228.1	140.3	350.4
11/18/2012	DPin	<i>E. coli</i>	49	24	10	4351.7	2762.3	6500.4
11/18/2012	DPout	<i>E. coli</i>	9	0	10	97.9	46.8	183.6
11/18/2012	B1	<i>E. coli</i>	6	1	10	73.8	32.4	144
11/18/2012	B2	<i>E. coli</i>	2	0	10	20.2	2.6	71.3
11/18/2012	B3	<i>E. coli</i>	6	0	10	63.2	29	137.1
11/18/2012	DPin	Enterococci	49	47	50	4839.1	3260.7	9432.2
11/18/2012	DPout	Enterococci	16	6	100	26.2	17.2	38.5
11/18/2012	B1	Enterococci	6	2	100	8.4	3.7	15.3
11/18/2012	B2	Enterococci	15	1	100	18.7	10.8	30
11/18/2012	B3	Enterococci	4	0	100	4.1	1.7	9.5
11/26/2012	DPin	Coliforms	49	32	10	6866.7	4492.9	9744.1
11/26/2012	DPout	Coliforms	18	2	10	243.3	154.4	370.6
11/26/2012	B1	Coliforms	19	0	10	233.4	143.6	361.1
11/26/2012	B2	Coliforms	22	1	10	295.4	187.5	439.7
11/26/2012	B3	Coliforms	23	1	10	312.9	204.7	459.9
11/26/2012	DPin	<i>E. coli</i>	49	13	10	2359.3	1589.7	3600
11/26/2012	DPout	<i>E. coli</i>	2	0	10	20.2	2.6	71.3
11/26/2012	B1	<i>E. coli</i>	4	0	10	41.3	16.5	95.2
11/26/2012	B2	<i>E. coli</i>	3	0	10	30.6	6.9	89.4
11/26/2012	B3	<i>E. coli</i>	4	1	10	51.6	17.6	107.6
11/26/2012	DPin	Enterococci	43	24	50	345.6	266.6	443.5
11/26/2012	DPout	Enterococci	25	4	100	39.3	26.5	55.9
11/26/2012	B1	Enterococci	21	2	100	29.2	18.5	43.1
11/26/2012	B2	Enterococci	8	2	100	10.8	5.2	18.6
11/26/2012	B3	Enterococci	6	1	100	7.4	3.2	14.4
12/3/2012	DPin	Coliforms	49	25	10	4611.1	2927	6878.8
12/3/2012	DPout	Coliforms	18	1	10	230.7	141.9	356.9
12/3/2012	B1	Coliforms	28	2	10	425.7	286.9	606.9
12/3/2012	B2	Coliforms	28	1	10	410.3	276.5	587.9
12/3/2012	B3	Coliforms	27	7	10	480.8	333.4	661.1
12/3/2012	DPin	<i>E. coli</i>	43	12	10	1245.7	912.4	1678.4
12/3/2012	DPout	<i>E. coli</i>	4	0	10	41.3	16.5	95.2
12/3/2012	B1	<i>E. coli</i>	11	0	10	122.3	68.1	214
12/3/2012	B2	<i>E. coli</i>	8	1	10	96.9	44.5	171.6
12/3/2012	B3	<i>E. coli</i>	15	4	10	223	137.2	341.3
12/3/2012	DPin	Enterococci	49	31	50	1297.6	849	1882.9
12/3/2012	DPin	Enterococci	49	31	50	1297.6	849	1882.9
12/3/2012	DPout	Enterococci	47	8	100	150	104	211.8
12/3/2012	B1	Enterococci	30	3	100	48.7	33.8	68
12/3/2012	B2	Enterococci	24	3	100	35.9	24.2	51.9
12/3/2012	B3	Enterococci	18	2	100	24.3	15.4	37.1
12/10/2012	DPin	Coliforms	49	29	10	5794.3	3791.2	8471.7
12/10/2012	DPout	Coliforms	17	4	10	253	160.6	376.7

12/10/2012	B1	Coliforms	42	2	10	878.2	608.9	1219.1
12/10/2012	B2	Coliforms	38	5	10	771.2	549.8	1057.4
12/10/2012	B3	Coliforms	31	7	10	580.6	413.9	794.6
12/10/2012	DPin	<i>E. coli</i>	48	10	10	1789	1240.4	2577.8
12/10/2012	DPout	<i>E. coli</i>	3	1	10	40.9	11.6	90.7
12/10/2012	B1	<i>E. coli</i>	5	1	10	62.6	25.1	127.3
12/10/2012	B2	<i>E. coli</i>	15	0	10	174.9	100.8	285.5
12/10/2012	B3	<i>E. coli</i>	14	4	10	208.6	124.3	323
12/10/2012	DPin	Enterococci	49	41	50	2406.7	1621.7	3501.4
12/10/2012	DPout	Enterococci	30	9	100	58.8	41.9	79.5
12/10/2012	B1	Enterococci	38	10	100	88.6	64.9	118.3
12/10/2012	B2	Enterococci	36	10	100	80.1	58.7	106.4
12/10/2012	B3	Enterococci	29	6	100	51.2	35.5	70.7
12/18/2012	DPin	Coliforms	49	39	10	10462.4	7049.9	15090.3
12/18/2012	DPout	Coliforms	26	2	10	383.9	258.7	553.5
12/18/2012	B1	Coliforms	42	11	10	1137	832.8	1516.7
12/18/2012	B2	Coliforms	49	28	10	5475	3582.3	8044.5
12/18/2012	B3	Coliforms	44	7	10	1152.8	821.8	1580.7
12/18/2012	DPin	<i>E. coli</i>	49	16	10	2755.1	1856.5	4167.6
12/18/2012	DPout	<i>E. coli</i>	10	2	10	132.3	71	220.1
12/18/2012	B1	<i>E. coli</i>	10	1	10	121.1	65	210.9
12/18/2012	B2	<i>E. coli</i>	25	2	10	364.1	238.2	525.5
12/18/2012	B3	<i>E. coli</i>	9	1	10	108.9	56.3	194.9
12/18/2012	DPin	Enterococci	49	40	50	2239.7	1509.2	3228
12/18/2012	DPout	Enterococci	15	9	100	28.4	18.6	41.2
12/18/2012	B1	Enterococci	47	11	100	166.4	115.4	234
12/18/2012	B2	Enterococci	48	28	100	396.8	275.1	555.5
12/18/2012	B3	Enterococci	40	10	100	98.5	72.2	132.1
12/31/2012	DPin	Coliforms	49	38	20	4902	3303.1	7050.8
12/31/2012	DPout	Coliforms	49	20	20	1724	1094.4	2603.3
12/31/2012	B1	Coliforms	47	12	20	861.7	597.5	1211.1
12/31/2012	B2	Coliforms	46	10	20	733.6	523	1005.5
12/31/2012	B3	Coliforms	46	11	20	757.6	540.1	1039.1
12/31/2012	DPin	<i>E. coli</i>	48	13	20	1007.1	678.6	1420.1
12/31/2012	DPout	<i>E. coli</i>	23	1	20	156.5	102.4	230
12/31/2012	B1	<i>E. coli</i>	19	2	20	129.5	82.2	195.5
12/31/2012	B2	<i>E. coli</i>	16	2	20	106.7	63.6	163
12/31/2012	B3	<i>E. coli</i>	14	2	20	92.5	55.1	146.1
12/31/2012	DPin	Enterococci	16	9	50	59.9	39.2	85.4
12/31/2012	DPout	Enterococci	6	2	100	8.4	3.7	15.3
12/31/2012	B1	Enterococci	2	1	100	3	0.7	7.4
12/31/2012	B2	Enterococci	2	2	100	4.1	1.2	9
12/31/2012	B3	Enterococci	0	2	100	2	0.3	5.6
1/7/2013	DPin	Coliforms	49	37	20	4604.2	3102.5	6410
1/7/2013	DPout	Coliforms	28	1	20	205.2	138.3	294
1/7/2013	B1	Coliforms	23	1	20	156.5	102.4	230
1/7/2013	B2	Coliforms	18	0	20	109.1	67.1	169.5
1/7/2013	B3	Coliforms	13	1	20	79.8	46	131.9
1/7/2013	DPin	<i>E. coli</i>	49	18	20	1538	976.3	2356.2
1/7/2013	DPout	<i>E. coli</i>	8	0	20	43	22.3	84.4
1/7/2013	B1	<i>E. coli</i>	5	1	20	31.3	12.6	63.7
1/7/2013	B2	<i>E. coli</i>	2	0	20	10.1	1.3	35.7
1/7/2013	B3	<i>E. coli</i>	4	0	20	20.7	8.3	47.6
1/7/2013	DPout	Enterococci	24	4	50	74.7	50.3	106.6

1/7/2013	DPout	Enterococci	24	4	100	37.3	25.2	53.3
1/7/2013	B1	Enterococci	29	7	100	52.8	36.6	72.3
1/7/2013	B2	Enterococci	25	2	100	36.4	23.8	52.6
1/7/2013	B3	Enterococci	23	0	100	29.9	19	44.4
1/14/2013	DPin	Coliforms	49	48	20	12098	7197.5	12098
1/14/2013	DPout	Coliforms	28	0	20	197.5	129.3	285.2
1/14/2013	B1	Coliforms	49	28	20	2737.5	1791.2	4022.3
1/14/2013	B2	Coliforms	48	12	20	967.5	651.9	1397.3
1/14/2013	B3	Coliforms	46	10	20	733.6	523	1005.5
1/14/2013	DPin	<i>E. coli</i>	49	47	20	12097.9	8151.9	23580.5
1/14/2013	DPout	<i>E. coli</i>	9	0	20	49	23.4	91.8
1/14/2013	B1	<i>E. coli</i>	49	19	20	1627.7	1033.2	2490.4
1/14/2013	B2	<i>E. coli</i>	27	3	20	209.8	141.4	298.5
1/14/2013	B3	<i>E. coli</i>	21	3	20	152.6	96.8	223.9
1/14/2013	DPin	Enterococci	48	48	50	2022.3	1481.2	2647
1/14/2013	DPout	Enterococci	10	5	100	16.6	9.6	26.8
1/14/2013	B1	Enterococci	38	15	100	100.8	75.8	132.1
1/14/2013	B2	Enterococci	31	9	100	61.6	43.9	83.3
1/14/2013	B3	Enterococci	37	5	100	73.3	52.2	100.1
1/20/2013	DPin	Coliforms	49	37	20	4604.2	3102.5	6410
1/20/2013	DPout	Coliforms	49	36	20	4332.2	2919.2	6226.9
1/20/2013	B1	Coliforms	49	20	20	1724	1094.4	2603.3
1/20/2013	B2	Coliforms	49	15	20	1306.3	854.7	1992.3
1/20/2013	B3	Coliforms	49	12	20	1123.4	735.1	1717.7
1/20/2013	DPin	<i>E. coli</i>	49	18	20	1538	976.3	2356.2
1/20/2013	DPout	<i>E. coli</i>	37	9	20	409.9	300.2	547
1/20/2013	B1	<i>E. coli</i>	31	2	20	247.7	171.8	346.6
1/20/2013	B2	<i>E. coli</i>	26	3	20	199.3	134.3	282.5
1/20/2013	B3	<i>E. coli</i>	29	2	20	224	150.9	316.8
1/20/2013	DPin	Enterococci	48	28	50	793.6	550.3	1110.9
1/20/2013	DPout	Enterococci	46	35	100	343.3	264.8	439.5
1/20/2013	B1	Enterococci	24	11	100	47.5	33.9	64.7
1/20/2013	B2	Enterococci	19	7	100	32.4	21.8	46.5
1/20/2013	B3	Enterococci	6	1	100	7.4	3.2	14.4
1/27/2013	DPin	Coliforms	49	47	20	12097.9	8151.9	23580.5
1/27/2013	DPout	Coliforms	31	2	20	247.7	171.8	346.6
1/27/2013	B1	Coliforms	30	5	20	260.2	180.4	361.1
1/27/2013	B2	Coliforms	23	1	20	156.5	102.4	230
1/27/2013	B3	Coliforms	21	1	20	139.3	91.1	206.3
1/27/2013	DPin	<i>E. coli</i>	38	7	20	408.1	291	551.6
1/27/2013	DPout	<i>E. coli</i>	5	1	20	31.3	12.6	63.7
1/27/2013	B1	<i>E. coli</i>	7	2	20	48	22.1	84.7
1/27/2013	B2	<i>E. coli</i>	2	0	20	10.1	1.3	35.7
1/27/2013	B3	<i>E. coli</i>	4	0	20	20.7	8.3	47.6
1/27/2013	DPin	Enterococci	49	29	50	1158.9	758.2	1694.3
1/27/2013	DPout	Enterococci	7	2	100	9.6	4.4	16.9
1/27/2013	B1	Enterococci	5	0	100	5.2	2.3	11.9
1/27/2013	B2	Enterococci	4	2	100	6.2	2.4	12.2
1/27/2013	B3	Enterococci	4	1	100	5.2	1.8	10.8

FIB concentrations in the stream bed sediments:

Date	Site	Analyte	Positive Wells		Volume	MPN/gram dry sediment			Moisture(%)
			Large	Small		Mean	Lower	Upper	
2/6/2012	DPout	Coliforms	49	34	50	1498.2	1068.1	2128.6	41.3
2/6/2012	B1	Coliforms	49	36	50	1583.3	1066.9	2275.8	37.5
2/6/2012	B2	Coliforms	49	20	50	579.0	367.6	874.4	31.9
2/6/2012	B3	Coliforms	49	43	50	2713.2	1775.3	4033.8	40.5
2/6/2012	DPout	<i>E. coli</i>	32	4	50	108.1	75	150.1	41.3
2/6/2012	B1	<i>E. coli</i>	48	22	50	545.7	378.5	773.3	37.5
2/6/2012	B2	<i>E. coli</i>	8	1	50	16.3	7.5	28.8	31.9
2/6/2012	B3	<i>E. coli</i>	39	8	50	169.7	121.1	228.7	40.5
2/6/2012	DPout	Enterococci	3	3	100	6.0	2.3	11.8	41.3
2/6/2012	B1	Enterococci	8	9	50	33.8	20.8	52.2	37.5
2/6/2012	B2	Enterococci	3	5	100	6.9	3.1	12.9	31.9
2/6/2012	B3	Enterococci	9	11	100	21.1	13.5	31.3	40.5
2/13/2012	DPout	Coliforms	49	47	30	22096.4	14889.4	43069.4	79.1
2/13/2012	B1	Coliforms	49	29	30	2904.4	1900.4	4246.5	62.0
2/13/2012	B2	Coliforms	47	11	30	1155.6	801.3	1624.8	72.6
2/13/2012	B3	Coliforms	26	4	30	145.8	98.4	206.6	46.0
2/13/2012	DPout	<i>E. coli</i>	31	9	30	562.2	400.9	760.6	79.1
2/13/2012	B1	<i>E. coli</i>	34	11	30	374.9	274.6	493.9	62.0
2/13/2012	B2	<i>E. coli</i>	20	0	30	172.9	109.8	264.6	72.6
2/13/2012	B3	<i>E. coli</i>	5	1	30	22.1	8.9	44.9	46.0
2/13/2012	DPout	Enterococci	4	5	100	25.5	12.4	46.4	79.1
2/13/2012	B1	Enterococci	10	1	100	18.2	9.8	31.8	62.0
2/13/2012	B2	Enterococci	8	2	100	22.5	10.9	38.8	72.6
2/13/2012	B3	Enterococci	3	0	100	3.3	0.8	9.5	46.0
2/27/2012	DPout	Coliforms	49	17	50	612.5	400.8	939.1	45.7
2/27/2012	B1	Coliforms	49	44	50	4141.6	2709.9	6274.8	57.1
2/27/2012	B2	Coliforms	49	38	50	2064.0	1390.8	2968.8	45.7
2/27/2012	B3	Coliforms	49	45	50	3850.9	2594.8	6021.1	48.6
2/27/2012	DPout	<i>E. coli</i>	9	4	50	29.9	16.2	49.4	45.7
2/27/2012	B1	<i>E. coli</i>	38	7	50	217.6	155.2	294.2	57.1
2/27/2012	B2	<i>E. coli</i>	41	11	50	225.5	165.2	300.4	45.7
2/27/2012	B3	<i>E. coli</i>	45	13	50	329.6	234.9	444.3	48.6
2/27/2012	DPout	Enterococci	8	2	100	11.4	5.5	19.6	45.7
2/27/2012	B1	Enterococci	3	1	100	5.5	1.7	12.2	57.1
2/27/2012	B2	Enterococci	2	1	100	3.2	0.8	7.8	45.7
2/27/2012	B3	Enterococci	2	1	100	3.3	0.8	8.3	48.6
3/6/2012	DPout	Coliforms	49	44	50	2701.0	1767.4	4092.3	34.3
3/6/2012	B1	Coliforms	49	40	50	2357.6	1588.7	3397.9	45.7
3/6/2012	B2	Coliforms	49	38	50	1634.0	1101	2350.3	31.4
3/6/2012	B3	Coliforms	49	46	50	4181.7	2572.8	6947.9	45.7
3/6/2012	DPout	<i>E. coli</i>	35	10	50	132.8	97.3	176	34.3
3/6/2012	B1	<i>E. coli</i>	45	8	50	268.2	191.2	371.4	45.7
3/6/2012	B2	<i>E. coli</i>	42	8	50	174.3	124.3	236.8	31.4
3/6/2012	B3	<i>E. coli</i>	49	25	50	970.7	616.3	1448.3	45.7
3/6/2012	DPout	Enterococci	29	9	100	48.8	34.8	66.1	34.3
3/6/2012	B1	Enterococci	9	3	100	13.8	7.2	23	45.7
3/6/2012	B2	Enterococci	8	2	100	9.0	4.4	15.5	31.4
3/6/2012	B3	Enterococci	15	5	100	24.7	15.7	37.1	45.7
3/12/2012	DPin	Coliforms	49	37	50	1674.3	1128.2	2331	26.7

3/12/2012	DPout	Coliforms	49	27	50	1034.4	676.8	1527.1	33.3
3/12/2012	B1	Coliforms	49	22	50	860.7	546.4	1260.2	40.0
3/12/2012	B2	Coliforms	49	29	50	1007.7	659.4	1473.4	40.0
3/12/2012	B3	Coliforms	48	2	50	231.4	156	335.4	23.3
3/12/2012	DPin	<i>E. coli</i>	49	23	50	746.5	473.9	1125.3	26.7
3/12/2012	DPout	<i>E. coli</i>	27	3	50	83.9	56.5	119.4	33.3
3/12/2012	B1	<i>E. coli</i>	21	7	50	79.8	53.8	113.4	40.0
3/12/2012	B2	<i>E. coli</i>	36	3	50	114.2	79.2	157.1	40.0
3/12/2012	B3	<i>E. coli</i>	17	2	50	39.7	24.5	61	23.3
3/12/2012	DPin	Enterococci	31	6	100	51.2	35.6	70.6	26.7
3/12/2012	DPout	Enterococci	5	4	100	9.4	4.3	16.9	33.3
3/12/2012	B1	Enterococci	6	4	100	11.8	5.9	20.6	40.0
3/12/2012	B2	Enterococci	15	5	100	26.1	16.6	39.2	40.0
3/12/2012	B3	Enterococci	9	3	100	11.4	6	19	23.3
3/19/2012	DPin	Coliforms	49	39	50	1902.3	1281.9	2743.8	26.7
3/19/2012	DPout	Coliforms	49	46	50	5296.8	3258.8	8800.7	50.0
3/19/2012	B1	Coliforms	49	32	50	1445.6	945.9	2051.4	36.7
3/19/2012	B2	Coliforms	49	23	50	966.1	613.2	1456.3	50.0
3/19/2012	B3	Coliforms	45	17	50	394.0	288.6	524	43.3
3/19/2012	DPin	<i>E. coli</i>	47	8	50	272.7	189.1	385.1	26.7
3/19/2012	DPout	<i>E. coli</i>	41	6	50	248.7	177.4	337	50.0
3/19/2012	B1	<i>E. coli</i>	27	3	50	88.3	59.5	125.7	36.7
3/19/2012	B2	<i>E. coli</i>	26	8	50	111.4	77.3	153.9	50.0
3/19/2012	B3	<i>E. coli</i>	20	3	50	67.8	43.1	100.5	43.3
3/19/2012	DPin	Enterococci	38	12	100	84.9	62.2	112	26.7
3/19/2012	DPout	Enterococci	3	2	100	6.8	2.3	14.2	50.0
3/19/2012	B1	Enterococci	7	1	100	8.9	4.2	16.5	36.7
3/19/2012	B2	Enterococci	8	1	100	11.4	5.3	20.3	50.0
3/19/2012	B3	Enterococci	13	2	100	20.1	11.7	32.3	43.3
3/26/2012	DPin	Coliforms	49	40	30	3393.5	2286.7	4891	26.7
3/26/2012	DPout	Coliforms	49	30	30	1858.0	1215.8	2664.3	26.7
3/26/2012	B1	Coliforms	49	44	30	6471.4	4234.2	9804.4	40.0
3/26/2012	B2	Coliforms	49	47	30	8065.2	5434.6	15720.3	46.7
3/26/2012	B3	Coliforms	49	41	30	4011.1	2702.8	5835.7	33.3
3/26/2012	DPin	<i>E. coli</i>	32	8	30	189.9	135.4	258.4	26.7
3/26/2012	DPout	<i>E. coli</i>	23	2	30	99.0	64.9	144.5	26.7
3/26/2012	B1	<i>E. coli</i>	49	15	30	1088.5	712.3	1660.3	40.0
3/26/2012	B2	<i>E. coli</i>	49	30	30	2043.8	1337.3	2930.7	46.7
3/26/2012	B3	<i>E. coli</i>	47	9	30	517.5	358.8	729.1	33.3
3/26/2012	DPin	Enterococci	10	6	100	16.1	9.7	25	26.7
3/26/2012	DPout	Enterococci	8	2	100	9.8	4.8	17	26.7
3/26/2012	B1	Enterococci	6	7	100	17.3	9.7	27.8	40.0
3/26/2012	B2	Enterococci	4	2	100	6.2	2.4	12.2	46.7
3/26/2012	B3	Enterococci	39	8	100	88.4	63	119.2	33.3
4/2/2012	DPin	Coliforms	36	8	25	276.0	196.8	368.6	26.7
4/2/2012	DPout	Coliforms	49	42	25	5472.2	3580.5	7985.5	36.7
4/2/2012	B1	Coliforms	49	41	25	4813.3	3243.4	7002.8	33.3
4/2/2012	B2	Coliforms	49	43	25	5952.0	3894.5	8849	36.7
4/2/2012	B3	Coliforms	49	30	25	2335.8	1528.3	3349.4	30.0
4/2/2012	DPin	<i>E. coli</i>	1	1	25	7.3	1	21.6	26.7
4/2/2012	DPout	<i>E. coli</i>	37	2	25	282.1	195.6	387.3	36.7
4/2/2012	B1	<i>E. coli</i>	20	2	25	110.0	69.8	164.7	33.3
4/2/2012	B2	<i>E. coli</i>	49	33	25	3061.1	2002.9	4416.4	36.7
4/2/2012	B3	<i>E. coli</i>	20	3	25	109.8	69.8	162.7	30.0

4/2/2012	DPin	Enterococci	4	1	100	4.7	1.7	9.9	26.7
4/2/2012	DPout	Enterococci	2	4	100	6.4	2.5	12.8	36.7
4/2/2012	B1	Enterococci	2	0	100	2.0	0.3	7.1	33.3
4/2/2012	B2	Enterococci	5	1	100	6.6	2.7	13.4	36.7
4/2/2012	B3	Enterococci	3	1	100	3.9	1.2	8.7	30.0
4/9/2012	DPin	Coliforms	49	47	25	8415.9	5670.9	16403.9	23.3
4/9/2012	DPout	Coliforms	49	47	25	27652.3	18632.9	53898.3	76.7
4/9/2012	B1	Coliforms	49	47	25	17596.9	11857.3	34299	63.3
4/9/2012	B2	Coliforms	49	44	25	9557.7	6253.6	14480.4	56.7
4/9/2012	B3	Coliforms	49	42	25	4951.0	3239.5	7225	30.0
4/9/2012	DPin	<i>E. coli</i>	35	9	25	258.4	184.3	343.5	23.3
4/9/2012	DPout	<i>E. coli</i>	49	18	25	3515.4	2231.5	5385.5	76.7
4/9/2012	B1	<i>E. coli</i>	45	14	25	1111.6	814.2	1499.7	63.3
4/9/2012	B2	<i>E. coli</i>	48	9	25	1059.4	734.7	1507.4	56.7
4/9/2012	B3	<i>E. coli</i>	30	6	25	204.6	146	281.9	30.0
4/9/2012	DPin	Enterococci	17	4	100	22.0	14	32.8	23.3
4/9/2012	DPout	Enterococci	2	1	100	8.6	2	21.2	76.7
4/9/2012	B1	Enterococci	6	15	100	40.9	26.8	59.3	63.3
4/9/2012	B2	Enterococci	0	1	100	1.5	0	5.7	56.7
4/9/2012	B3	Enterococci	0	4	100	3.8	1.1	8.5	30.0
4/16/2012	DPin	Coliforms	43	8	15	644.8	459.7	879.3	23.3
4/16/2012	DPout	Coliforms	49	47	15	21507.3	14492.2	41921	50.0
4/16/2012	B1	Coliforms	49	37	15	6821.0	4596.3	9496.4	40.0
4/16/2012	B2	Coliforms	49	21	15	2865.9	1819.2	4356.5	43.3
4/16/2012	B3	Coliforms	47	12	15	1094.2	758.7	1538	30.0
4/16/2012	DPin	<i>E. coli</i>	8	2	15	62.5	30	108	23.3
4/16/2012	DPout	<i>E. coli</i>	47	13	15	1586.9	1100.3	2226.3	50.0
4/16/2012	B1	<i>E. coli</i>	12	3	15	125.4	69.9	200.4	40.0
4/16/2012	B2	<i>E. coli</i>	16	0	15	148.2	88.4	238.2	43.3
4/16/2012	B3	<i>E. coli</i>	11	2	15	92.0	49.5	149.7	30.0
4/16/2012	DPin	Enterococci	34	2	100	50.1	34.7	69.6	23.3
4/16/2012	DPout	Enterococci	1	0	100	1.3	0.2	7.4	50.0
4/16/2012	B1	Enterococci	4	0	100	4.6	1.9	10.6	40.0
4/16/2012	B2	Enterococci	5	0	100	6.1	2.8	14.1	43.3
4/16/2012	B3	Enterococci	0	2	100	1.9	0.3	5.4	30.0
4/25/2012	DPin	Coliforms	49	43	15	7853.4	5138.5	11675.7	20.0
4/25/2012	DPout	Coliforms	49	47	15	11521.8	7763.7	22457.7	6.7
4/25/2012	B1	Coliforms	49	47	15	15362.4	10351.6	29943.6	30.0
4/25/2012	B2	Coliforms	49	46	15	13938.8	8575.7	23159.5	36.7
4/25/2012	B3	Coliforms	49	44	15	10354.1	6774.7	15687.1	33.3
4/25/2012	DPin	<i>E. coli</i>	19	4	15	158.2	100.5	232.2	20.0
4/25/2012	DPout	<i>E. coli</i>	43	7	15	514.6	366.9	701.2	6.7
4/25/2012	B1	<i>E. coli</i>	35	3	15	396.5	274.9	547.2	30.0
4/25/2012	B2	<i>E. coli</i>	33	8	15	460.9	328.6	626.3	36.7
4/25/2012	B3	<i>E. coli</i>	37	1	15	433.1	300.3	597.4	33.3
4/25/2012	DPin	Enterococci	6	3	100	7.9	3.7	14.1	20.0
4/25/2012	DPout	Enterococci	8	2	100	7.7	3.8	13.3	6.7
4/25/2012	B1	Enterococci	48	48	100	963.0	705.4	1260.5	30.0
4/25/2012	B2	Enterococci	32	8	100	66.0	47.1	89.8	36.7
4/25/2012	B3	Enterococci	12	3	100	16.9	9.4	27	33.3
5/3/2012	DPin	Coliforms	47	10	10	1339.3	928.6	1886.3	20.0
5/3/2012	DPout	Coliforms	45	10	10	1230.9	877.6	1672.9	26.7
5/3/2012	B1	Coliforms	49	23	10	3570.3	2266.3	5382	23.3
5/3/2012	B2	Coliforms	49	21	10	3846.3	2441.5	5846.9	36.7

5/3/2012	B3	Coliforms	49	26	10	4440.4	2818.6	6558.7	26.7
5/3/2012	DPin	<i>E. coli</i>	11	2	10	120.8	65	196.5	20.0
5/3/2012	DPout	<i>E. coli</i>	1	1	10	18.3	2.3	53.9	26.7
5/3/2012	B1	<i>E. coli</i>	9	10	10	181.8	115.4	271.3	23.3
5/3/2012	B2	<i>E. coli</i>	12	1	10	154.1	85.8	259.2	36.7
5/3/2012	B3	<i>E. coli</i>	11	2	10	131.7	70.9	214.3	26.7
5/3/2012	DPin	Enterococci	29	7	100	44.0	30.5	60.3	20.0
5/3/2012	DPout	Enterococci	3	0	100	2.8	0.7	8.1	26.7
5/3/2012	B1	Enterococci	2	1	100	2.6	0.7	6.5	23.3
5/3/2012	B2	Enterococci	2	13	100	16.2	9.9	25.3	36.7
5/3/2012	B3	Enterococci	0	4	100	3.6	1	8.1	26.7
5/10/2012	DPin	Coliforms	49	47	10	21039.7	14177.2	41009.6	23.3
5/10/2012	DPout	Coliforms	49	47	10	25469.2	17161.8	49643.2	36.7
5/10/2012	B1	Coliforms	48	17	10	2382.2	1651.8	3407.8	33.3
5/10/2012	B2	Coliforms	49	38	10	15082.9	10163.3	21694.8	56.7
5/10/2012	B3	Coliforms	40	5	10	779.5	555.8	1065.3	26.7
5/10/2012	DPin	<i>E. coli</i>	37	4	10	618.8	441.2	854.8	23.3
5/10/2012	DPout	<i>E. coli</i>	29	2	10	471.5	317.7	667	36.7
5/10/2012	B1	<i>E. coli</i>	3	1	10	40.9	11.6	90.7	33.3
5/10/2012	B2	<i>E. coli</i>	29	1	10	664.8	448.1	944.4	56.7
5/10/2012	B3	<i>E. coli</i>	17	3	10	218.6	134.6	331.4	26.7
5/10/2012	DPin	Enterococci	23	5	100	32.0	21.6	45.4	23.3
5/10/2012	DPout	Enterococci	20	5	100	33.2	21.7	48.2	36.7
5/10/2012	B1	Enterococci	16	1	100	20.1	12.4	31.8	33.3
5/10/2012	B2	Enterococci	28	26	100	127.1	98.1	159.9	56.7
5/10/2012	B3	Enterococci	13	2	100	15.5	9.1	25	26.7
5/16/2012	DPin	Coliforms	49	27	10	5172.1	3384.1	7635.6	33.3
5/16/2012	DPout	Coliforms	49	47	10	25469.2	17161.8	49643.2	36.7
5/16/2012	B1	Coliforms	48	19	10	2478.6	1670.1	3478.1	30.0
5/16/2012	B2	Coliforms	49	44	10	25885.3	16936.7	39217.7	60.0
5/16/2012	B3	Coliforms	49	32	10	6539.7	4279	9280.1	30.0
5/16/2012	DPin	<i>E. coli</i>	38	3	10	727.3	518.5	1009.7	33.3
5/16/2012	DPout	<i>E. coli</i>	26	8	10	498.6	345.7	688.7	36.7
5/16/2012	B1	<i>E. coli</i>	8	1	10	92.3	42.4	163.5	30.0
5/16/2012	B2	<i>E. coli</i>	24	3	10	598.7	403.4	864.4	60.0
5/16/2012	B3	<i>E. coli</i>	11	2	10	138.0	74.2	224.5	30.0
5/16/2012	DPin	Enterococci	40	4	100	83.3	59.4	114.6	33.3
5/16/2012	DPout	Enterococci	27	7	100	50.6	35.1	69.6	36.7
5/16/2012	B1	Enterococci	22	6	100	34.7	23.4	48.9	30.0
5/16/2012	B2	Enterococci	23	29	100	120.8	93.4	152.7	60.0
5/16/2012	B3	Enterococci	10	7	100	18.0	11.1	27.5	30.0
5/23/2012	DPin	Coliforms	49	25	10	3842.6	2439.2	5732.4	20.0
5/23/2012	DPout	Coliforms	49	40	10	10180.6	6860	14672.8	26.7
5/23/2012	B1	Coliforms	49	45	10	16503.7	11120.7	25804.5	30.0
5/23/2012	B2	Coliforms	49	45	10	38508.7	25948.3	60210.5	70.0
5/23/2012	B3	Coliforms	49	42	10	12377.6	8098.7	18062.5	30.0
5/23/2012	DPin	<i>E. coli</i>	16	4	10	198.2	122	298.1	20.0
5/23/2012	DPout	<i>E. coli</i>	21	2	10	265.2	168.4	391.8	26.7
5/23/2012	B1	<i>E. coli</i>	29	4	10	457.0	316.9	639.9	30.0
5/23/2012	B2	<i>E. coli</i>	28	1	10	911.8	614.5	1306.5	70.0
5/23/2012	B3	<i>E. coli</i>	21	1	10	265.2	173.6	393	30.0
5/23/2012	DPin	Enterococci	28	5	100	39.4	27.4	55	20.0
5/23/2012	DPout	Enterococci	13	0	100	13.5	7.8	22.9	26.7
5/23/2012	B1	Enterococci	28	13	100	57.3	42	76.2	30.0

5/23/2012	B2	Enterococci	37	33	100	320.4	253.6	393.4	70.0
5/23/2012	B3	Enterococci	43	9	100	109.0	77.8	148.1	30.0
5/30/2012	DPin	Coliforms	49	18	10	2674.7	1697.9	4097.7	23.3
5/30/2012	DPout	Coliforms	49	29	10	5518.4	3610.7	8068.3	30.0
5/30/2012	B1	Coliforms	49	22	10	3688.8	2341.6	5400.4	30.0
5/30/2012	B2	Coliforms	49	41	10	26740.7	18018.7	38904.5	70.0
5/30/2012	B3	Coliforms	49	47	10	21996.1	14821.6	42873.7	26.7
5/30/2012	DPin	<i>E. coli</i>	19	1	10	214.1	131.7	327.4	23.3
5/30/2012	DPout	<i>E. coli</i>	10	3	10	136.7	73.5	224.3	30.0
5/30/2012	B1	<i>E. coli</i>	42	8	10	996.2	710.2	1352.9	30.0
5/30/2012	B2	<i>E. coli</i>	24	6	10	893.3	602	1252.3	70.0
5/30/2012	B3	<i>E. coli</i>	48	47	10	8732.8	6396.2	11321.7	26.7
5/30/2012	DPin	Enterococci	30	4	100	43.8	30.4	61	23.3
5/30/2012	DPout	Enterococci	22	3	100	30.8	20.1	45	30.0
5/30/2012	B1	Enterococci	32	4	100	53.0	36.7	73.6	30.0
5/30/2012	B2	Enterococci	16	2	100	47.3	28.3	72.5	70.0
5/30/2012	B3	Enterococci	49	31	100	589.8	386	856	26.7
6/4/2012	DPin	Coliforms	49	36	10	7534.3	5076.8	10829.4	23.3
6/4/2012	DPout	Coliforms	49	47	10	24195.7	16303.7	47161	33.3
6/4/2012	B1	Coliforms	49	34	10	7701.0	5490	10940.3	33.3
6/4/2012	B2	Coliforms	48	48	10	16852.7	12343.4	22058.4	60.0
6/4/2012	B3	Coliforms	49	42	10	12996.5	8503.6	18965.6	33.3
6/4/2012	DPin	<i>E. coli</i>	44	12	10	1160.3	827.3	1547.1	23.3
6/4/2012	DPout	<i>E. coli</i>	26	3	10	398.6	268.6	565	33.3
6/4/2012	B1	<i>E. coli</i>	13	1	10	159.6	91.9	263.7	33.3
6/4/2012	B2	<i>E. coli</i>	46	15	10	2874.5	2049.4	3925	60.0
6/4/2012	B3	<i>E. coli</i>	18	3	10	255.9	157.4	383.6	33.3
6/4/2012	DPin	Enterococci	34	10	100	63.3	45.2	83.7	23.3
6/4/2012	DPout	Enterococci	28	7	100	50.4	35	69.1	33.3
6/4/2012	B1	Enterococci	13	3	100	18.3	10.5	28.8	33.3
6/4/2012	B2	Enterococci	15	5	100	39.2	24.9	58.7	60.0
6/4/2012	B3	Enterococci	15	3	100	21.1	12.6	32.6	33.3
6/11/2012	DPin	Coliforms	47	12	10	1566.6	1086.3	2202.1	26.7
6/11/2012	DPout	Coliforms	49	47	10	25469.2	17161.8	49643.2	36.7
6/11/2012	B1	Coliforms	49	40	10	11198.7	7546	16140	33.3
6/11/2012	B2	Coliforms	49	46	10	24828.6	15275.4	41252.9	46.7
6/11/2012	B3	Coliforms	49	40	10	11198.7	7546	16140	33.3
6/11/2012	DPin	<i>E. coli</i>	4	0	10	37.5	15.1	86.6	26.7
6/11/2012	DPout	<i>E. coli</i>	19	3	10	286.1	181.6	423.1	36.7
6/11/2012	B1	<i>E. coli</i>	24	1	10	331.0	216.6	481.3	33.3
6/11/2012	B2	<i>E. coli</i>	24	0	10	396.3	259.3	583	46.7
6/11/2012	B3	<i>E. coli</i>	17	1	10	215.7	128.5	337.1	33.3
6/11/2012	DPin	Enterococci	3	7	100	9.4	4.7	16.7	26.7
6/11/2012	DPout	Enterococci	15	6	100	26.0	16.6	38.5	36.7
6/11/2012	B1	Enterococci	21	2	100	29.2	18.5	43.1	33.3
6/11/2012	B2	Enterococci	2	3	100	6.4	2	13.3	46.7
6/11/2012	B3	Enterococci	6	0	100	6.3	2.9	13.7	33.3
6/18/2012	DPin	Coliforms	49	34	5	13393.0	9547.9	19026.7	23.3
6/18/2012	DPout	Coliforms	49	34	5	16212.6	11557.9	23032.3	36.7
6/18/2012	B1	Coliforms	49	20	5	6896.0	4377.4	10413.2	33.3
6/18/2012	B2	Coliforms	49	15	5	5225.0	3418.8	7969	33.3
6/18/2012	B3	Coliforms	43	11	5	2307.0	1689.8	3109.8	30.0
6/18/2012	DPin	<i>E. coli</i>	30	3	5	847.7	587.9	1183	23.3
6/18/2012	DPout	<i>E. coli</i>	23	2	5	687.8	450.2	1003.6	36.7

6/18/2012	B1	<i>E. coli</i>	12	3	5	338.8	188.6	540.8	33.3
6/18/2012	B2	<i>E. coli</i>	3	0	5	61.2	13.8	178.8	33.3
6/18/2012	B3	<i>E. coli</i>	6	0	5	120.4	55.3	261.2	30.0
6/18/2012	DPin	Enterococci	19	21	100	44.5	32.7	58.6	23.3
6/18/2012	DPout	Enterococci	49	32	100	722.8	473	1025.7	36.7
6/18/2012	B1	Enterococci	33	2	100	54.8	38	76.4	33.3
6/18/2012	B2	Enterococci	13	0	100	14.8	8.5	25.1	33.3
6/18/2012	B3	Enterococci	10	5	100	15.8	9.2	25.6	30.0
6/25/2012	DPin	Coliforms	31	5	2	2275.4	1578	3148.8	20.0
6/25/2012	DPout	Coliforms	49	44	2	91360.0	59776.5	138415.3	43.3
6/25/2012	B1	Coliforms	49	44	2	86284.4	56455.6	130725.6	40.0
6/25/2012	B2	Coliforms	49	45	2	216611.3	145958.8	338683.8	73.3
6/25/2012	B3	Coliforms	49	47	2	302446.3	203796.3	589512.5	73.3
6/25/2012	DPin	<i>E. coli</i>	4	1	2	215.0	73.4	448.4	20.0
6/25/2012	DPout	<i>E. coli</i>	28	1	2	2413.5	1626.5	3458.3	43.3
6/25/2012	B1	<i>E. coli</i>	32	36	2	6655.6	5264.5	8120.6	40.0
6/25/2012	B2	<i>E. coli</i>	29	4	2	5997.5	4158.8	8397.5	73.3
6/25/2012	B3	<i>E. coli</i>	38	4	2	9363.8	6675	12860	73.3
6/25/2012	DPin	Enterococci	3	0	100	2.6	0.6	7.5	20.0
6/25/2012	DPout	Enterococci	41	21	100	163.3	126	208.3	43.3
6/25/2012	B1	Enterococci	39	20	100	133.7	103.2	171.9	40.0
6/25/2012	B2	Enterococci	39	12	100	246.0	180.3	326.5	73.3
6/25/2012	B3	Enterococci	37	13	100	227.8	166.8	300.5	73.3
7/2/2012	DPin	Coliforms	49	43	5	26250.9	17175.9	39027.3	28.2
7/2/2012	DPout	Coliforms	49	45	5	32435.9	21856.3	50715.4	28.8
7/2/2012	B1	Coliforms	49	47	5	46709.8	31474.4	91044.5	30.9
7/2/2012	B2	Coliforms	49	47	5	54008.3	36392.2	105270.1	40.3
7/2/2012	B3	Coliforms	49	18	5	5584.9	3545.2	8556.2	26.6
7/2/2012	DPin	<i>E. coli</i>	19	3	5	504.7	320.4	746.4	28.2
7/2/2012	DPout	<i>E. coli</i>	37	6	5	1411.5	1006.3	1920.1	28.8
7/2/2012	B1	<i>E. coli</i>	38	7	5	1575.7	1123.4	2129.8	30.9
7/2/2012	B2	<i>E. coli</i>	18	2	5	543.1	344.7	827.3	40.3
7/2/2012	B3	<i>E. coli</i>	8	0	5	156.2	80.8	306.4	26.6
7/2/2012	DPin	Enterococci	49	25	100	428.1	271.8	638.8	28.2
7/2/2012	DPout	Enterococci	34	19	100	85.5	64.3	110.5	28.8
7/2/2012	B1	Enterococci	12	13	100	27.6	18.7	39.2	30.9
7/2/2012	B2	Enterococci	4	5	100	10.4	5.1	18.9	40.3
7/2/2012	B3	Enterococci	11	2	100	13.2	7.1	21.5	26.6
7/9/2012	DPin	Coliforms	37	6	2	3462.4	2468.4	4709.9	27.4
7/9/2012	DPout	Coliforms	49	47	2	433614.7	292181.1	845179.3	81.4
7/9/2012	B1	Coliforms	49	17	2	14047.8	9191.7	21538	31.0
7/9/2012	B2	Coliforms	49	15	2	12123.0	7932.3	18489.6	28.2
7/9/2012	B3	Coliforms	47	4	2	5730.0	3860.9	8193	23.8
7/9/2012	DPin	<i>E. coli</i>	3	1	2	187.8	53.3	416.5	27.4
7/9/2012	DPout	<i>E. coli</i>	29	2	2	8026.9	5408.7	11354.9	81.4
7/9/2012	B1	<i>E. coli</i>	8	0	2	415.3	214.9	814.6	31.0
7/9/2012	B2	<i>E. coli</i>	3	0	2	142.0	32.1	414.9	28.2
7/9/2012	B3	<i>E. coli</i>	2	0	2	88.4	11.4	312.1	23.8
7/9/2012	DPin	Enterococci	45	13	100	136.2	97.1	183.6	27.4
7/9/2012	DPout	Enterococci	6	1	100	26.5	11.5	51.7	81.4
7/9/2012	B1	Enterococci	32	2	100	50.3	34.9	70.5	31.0
7/9/2012	B2	Enterococci	7	1	100	7.9	3.7	14.5	28.2
7/9/2012	B3	Enterococci	10	0	100	9.6	5	17.6	23.8
7/16/2012	DPin	Coliforms	49	41	3	37522.0	25283.5	54590	28.7

7/16/2012	DPout	Coliforms	49	26	3	16379.6	10397.1	24193.5	33.7
7/16/2012	B1	Coliforms	49	38	3	30231.0	20370.4	43483.2	27.9
7/16/2012	B2	Coliforms	49	45	3	83352.1	56165	130325.7	53.8
7/16/2012	B3	Coliforms	49	27	3	17052.7	11157.6	25175.1	32.6
7/16/2012	DPin	<i>E. coli</i>	23	4	3	1105.4	744.7	1591	28.7
7/16/2012	DPout	<i>E. coli</i>	7	0	3	249.8	119.5	498.7	33.7
7/16/2012	B1	<i>E. coli</i>	25	2	3	1122.8	734.6	1620.5	27.9
7/16/2012	B2	<i>E. coli</i>	18	1	3	1109.7	682.6	1716.8	53.8
7/16/2012	B3	<i>E. coli</i>	5	0	3	171.8	75.5	393.7	32.6
7/16/2012	DPin	Enterococci	49	47	100	2263.4	1525.2	4411.7	28.7
7/16/2012	DPout	Enterococci	15	0	100	17.6	10.2	28.8	33.7
7/16/2012	B1	Enterococci	40	13	100	98.7	72.4	129.9	27.9
7/16/2012	B2	Enterococci	6	4	100	15.3	7.7	26.7	53.8
7/16/2012	B3	Enterococci	5	2	100	7.2	2.9	13.8	32.6
7/23/2012	DPin	Coliforms	49	17	3	8662.5	5668	13281.2	25.4
7/23/2012	DPout	Coliforms	49	38	3	32647.1	21998.4	46958.4	33.3
7/23/2012	B1	Coliforms	49	39	3	33630.4	22661.3	48506.3	30.9
7/23/2012	B2	Coliforms	49	40	3	33404.0	22508.6	48143.2	25.5
7/23/2012	B3	Coliforms	49	47	3	73823.6	49744.4	143893.2	27.2
7/23/2012	DPin	<i>E. coli</i>	6	0	3	188.2	86.4	408.3	25.4
7/23/2012	DPout	<i>E. coli</i>	2	2	3	134.9	38.3	298.1	33.3
7/23/2012	B1	<i>E. coli</i>	7	2	3	308.6	141.8	544.2	30.9
7/23/2012	B2	<i>E. coli</i>	6	0	3	188.5	86.6	409	25.5
7/23/2012	B3	<i>E. coli</i>	15	1	3	570.3	328.7	914.7	27.2
7/23/2012	DPin	Enterococci	19	5	100	26.6	17.5	38.8	25.4
7/23/2012	DPout	Enterococci	7	0	100	7.5	3.6	14.9	33.3
7/23/2012	B1	Enterococci	40	26	100	141.9	109.5	180.3	30.9
7/23/2012	B2	Enterococci	11	2	100	13.0	7	21.2	25.5
7/23/2012	B3	Enterococci	32	8	100	57.4	41	78.1	27.2
7/30/2012	DPin	Coliforms	49	31	3	20412.7	13356.1	29619.7	29.4
7/30/2012	DPout	Coliforms	48	9	3	5051.7	3502.7	7187.8	24.3
7/30/2012	B1	Coliforms	48	22	3	10880.1	7544	15416.1	39.0
7/30/2012	B2	Coliforms	49	47	3	199387.6	134352.8	388636.1	73.0
7/30/2012	B3	Coliforms	49	35	3	25893.1	17447.5	37253.1	29.9
7/30/2012	DPin	<i>E. coli</i>	1	0	3	31.4	1.7	172.8	29.4
7/30/2012	DPout	<i>E. coli</i>	4	0	3	121.2	48.5	279.4	24.3
7/30/2012	B1	<i>E. coli</i>	10	0	3	400.8	207.4	731.5	39.0
7/30/2012	B2	<i>E. coli</i>	35	4	3	5304.6	3677.9	7302.2	73.0
7/30/2012	B3	<i>E. coli</i>	10	2	3	419.6	225.3	698.1	29.9
7/30/2012	DPin	Enterococci	3	0	100	2.9	0.7	8.5	29.4
7/30/2012	DPout	Enterococci	31	7	100	51.1	36.5	70	24.3
7/30/2012	B1	Enterococci	6	4	100	11.6	5.8	20.3	39.0
7/30/2012	B2	Enterococci	18	40	100	187.6	148.4	232.2	73.0
7/30/2012	B3	Enterococci	10	8	100	19.0	12.1	29	29.9
8/7/2012	DPin	Coliforms	48	16	3	6291.1	4362.1	8907.7	19.4
8/7/2012	DPout	Coliforms	47	14	3	5496.4	3918.3	7613	25.2
8/7/2012	B1	Coliforms	49	12	3	6563.8	4294.8	10036	23.9
8/7/2012	B2	Coliforms	48	14	3	6258.6	4339.5	8981.7	25.5
8/7/2012	B3	Coliforms	48	17	3	7335.5	5086.4	10493.6	27.8
8/7/2012	DPin	<i>E. coli</i>	1	0	3	27.5	1.5	151.4	19.4
8/7/2012	DPout	<i>E. coli</i>	9	0	3	290.8	139.1	545.5	25.2
8/7/2012	B1	<i>E. coli</i>	7	1	3	248.9	114.2	456.9	23.9
8/7/2012	B2	<i>E. coli</i>	5	1	3	186.8	74.9	379.7	25.5
8/7/2012	B3	<i>E. coli</i>	4	0	3	127.2	50.9	293.2	27.8

8/7/2012	DPin	Enterococci	14	2	100	15.3	9.1	24.2	19.4
8/7/2012	DPout	Enterococci	10	1	100	10.8	5.8	18.9	25.2
8/7/2012	B1	Enterococci	35	8	100	63.4	45.2	84.5	23.9
8/7/2012	B2	Enterococci	27	3	100	37.6	25.4	53.5	25.5
8/7/2012	B3	Enterococci	27	2	100	37.3	25.3	53.1	27.8
8/13/2012	DPin	Coliforms	49	13	3	6794.2	4578	10367.2	22.8
8/13/2012	DPout	Coliforms	49	37	3	28500.2	19204.3	39678.1	28.2
8/13/2012	B1	Coliforms	48	22	3	8690.8	6026	12314.1	23.6
8/13/2012	B2	Coliforms	49	33	3	21127.3	13823.7	30481.6	23.5
8/13/2012	B3	Coliforms	49	39	3	31704.3	21363.4	45728.2	26.7
8/13/2012	DPin	<i>E. coli</i>	6	0	3	182.0	83.6	394.9	22.8
8/13/2012	DPout	<i>E. coli</i>	20	1	3	811.2	515.1	1228.7	28.2
8/13/2012	B1	<i>E. coli</i>	2	0	3	58.8	7.6	207.6	23.6
8/13/2012	B2	<i>E. coli</i>	13	2	3	497.6	286.9	796	23.5
8/13/2012	B3	<i>E. coli</i>	19	1	3	746.1	458.9	1140.7	26.7
8/13/2012	DPin	Enterococci	12	1	100	12.6	7.1	21.3	22.8
8/13/2012	DPout	Enterococci	14	4	100	19.4	11.6	30	28.2
8/13/2012	B1	Enterococci	30	2	100	41.1	27.8	58.2	23.6
8/13/2012	B2	Enterococci	28	9	100	46.7	33.4	63.7	23.5
8/13/2012	B3	Enterococci	24	2	100	31.4	21.2	45.6	26.7
8/20/2012	DPin	Coliforms	48	13	3	5748.3	3873.3	8105.6	22.1
8/20/2012	DPout	Coliforms	49	17	3	8385.4	5486.7	12856.3	22.9
8/20/2012	B1	Coliforms	49	41	3	37876.3	25522.2	55105.5	29.4
8/20/2012	B2	Coliforms	49	39	3	33025.3	22253.6	47633.6	29.6
8/20/2012	B3	Coliforms	49	27	3	15503.9	10144.2	22888.5	25.9
8/20/2012	DPin	<i>E. coli</i>	2	0	3	57.6	7.5	203.6	22.1
8/20/2012	DPout	<i>E. coli</i>	12	2	3	455.1	253.4	741.1	22.9
8/20/2012	B1	<i>E. coli</i>	12	4	3	569.7	328.4	901.2	29.4
8/20/2012	B2	<i>E. coli</i>	17	3	3	759.2	467.2	1150.6	29.6
8/20/2012	B3	<i>E. coli</i>	11	0	3	366.6	204.2	641.5	25.9
8/20/2012	DPin	Enterococci	30	2	100	40.3	27.3	57.1	22.1
8/20/2012	DPout	Enterococci	25	1	100	30.3	19.9	44.3	22.9
8/20/2012	B1	Enterococci	39	8	100	83.5	59.5	112.6	29.4
8/20/2012	B2	Enterococci	28	5	100	44.8	31.1	62.5	29.6
8/20/2012	B3	Enterococci	19	1	100	22.1	13.6	33.9	25.9
8/27/2012	DPin	Coliforms	39	7	3	2557.3	1823.2	3434.8	25.3
8/27/2012	DPout	Coliforms	49	32	3	24068.3	15748	34153.9	36.6
8/27/2012	B1	Coliforms	45	12	3	4452.8	3174.6	6035.3	28.2
8/27/2012	B2	Coliforms	49	27	3	15795.1	10334.7	23318.4	27.2
8/27/2012	B3	Coliforms	49	17	3	8139.1	5325.5	12478.7	20.6
8/27/2012	DPin	<i>E. coli</i>	1	0	3	29.7	1.6	163.3	25.3
8/27/2012	DPout	<i>E. coli</i>	21	2	3	1022.4	649.2	1510.4	36.6
8/27/2012	B1	<i>E. coli</i>	4	1	3	159.7	54.6	333.1	28.2
8/27/2012	B2	<i>E. coli</i>	8	1	3	295.9	135.9	524.1	27.2
8/27/2012	B3	<i>E. coli</i>	6	1	3	206.5	90.7	402.9	20.6
8/27/2012	DPin	Enterococci	9	0	100	8.7	4.2	16.5	25.3
8/27/2012	DPout	Enterococci	3	1	100	4.3	1.3	9.6	36.6
8/27/2012	B1	Enterococci	10	1	100	11.2	6.1	19.6	28.2
8/27/2012	B2	Enterococci	17	4	100	23.2	14.8	34.6	27.2
8/27/2012	B3	Enterococci	8	2	100	9.1	4.4	15.7	20.6
9/3/2012	DPin	Coliforms	49	22	3	11275.7	7157.5	16507.7	23.7
9/3/2012	DPout	Coliforms	49	25	3	14192.3	9009	21172.1	27.8
9/3/2012	B1	Coliforms	49	24	3	13056.4	8287.8	19503.2	25.9
9/3/2012	B2	Coliforms	49	29	3	17719.5	11593.9	25907.4	27.3

9/3/2012	B3	Coliforms	49	38	3	28429.5	19156.5	40892	23.4
9/3/2012	DPin	<i>E. coli</i>	9	2	3	349.1	173.8	590.2	23.7
9/3/2012	DPout	<i>E. coli</i>	6	0	3	194.6	89.3	422	27.8
9/3/2012	B1	<i>E. coli</i>	12	1	3	439.2	244.6	738.8	25.9
9/3/2012	B2	<i>E. coli</i>	13	2	3	523.6	301.9	837.7	27.3
9/3/2012	B3	<i>E. coli</i>	7	0	3	216.0	103.3	431.3	23.4
9/3/2012	DPin	Enterococci	38	4	100	65.4	46.7	89.9	23.7
9/3/2012	DPout	Enterococci	2	1	100	2.8	0.7	6.9	27.8
9/3/2012	B1	Enterococci	40	6	100	79.4	56.7	108.2	25.9
9/3/2012	B2	Enterococci	45	16	100	149.0	109.2	197.9	27.3
9/3/2012	B3	Enterococci	43	7	100	94.0	67	128.1	23.4
9/10/2012	DPin	Coliforms	47	12	3	5085.7	3526.4	7148.3	24.7
9/10/2012	DPout	Coliforms	49	23	3	12917.4	8199.5	19472.2	29.4
9/10/2012	B1	Coliforms	49	35	3	23592.3	15897.1	33942.8	23.1
9/10/2012	B2	Coliforms	49	23	3	11854.5	7524.8	17869.9	23.0
9/10/2012	B3	Coliforms	49	23	3	12737.1	8085	19200.3	28.4
9/10/2012	DPin	<i>E. coli</i>	7	0	3	219.8	105.1	438.9	24.7
9/10/2012	DPout	<i>E. coli</i>	4	1	3	162.3	55.5	338.6	29.4
9/10/2012	B1	<i>E. coli</i>	11	3	3	451.7	251.5	730.3	23.1
9/10/2012	B2	<i>E. coli</i>	7	0	3	215.1	102.9	429.4	23.0
9/10/2012	B3	<i>E. coli</i>	3	1	3	126.8	36.1	281.4	28.4
9/10/2012	DPin	Enterococci	13	1	100	14.2	8.2	23.4	24.7
9/10/2012	DPout	Enterococci	1	0	100	0.9	0.1	5.2	29.4
9/10/2012	B1	Enterococci	13	1	100	13.9	8	22.9	23.1
9/10/2012	B2	Enterococci	9	0	100	8.5	4.1	16	23.0
9/10/2012	B3	Enterococci	5	1	100	5.9	2.4	11.9	28.4
9/17/2012	DPin	Coliforms	44	8	3	3416.5	2435.7	4680	22.8
9/17/2012	DPout	Coliforms	46	10	3	4917.7	3506	6740.4	33.7
9/17/2012	B1	Coliforms	48	9	3	6137.6	4255.7	8733	37.7
9/17/2012	B2	Coliforms	49	19	3	9775.9	6205.5	14957.4	26.0
9/17/2012	B3	Coliforms	48	22	3	9037.9	6266.7	12806	26.6
9/17/2012	DPin	<i>E. coli</i>	15	1	3	537.8	309.9	862.6	22.8
9/17/2012	DPout	<i>E. coli</i>	4	0	3	138.5	55.4	319.1	33.7
9/17/2012	B1	<i>E. coli</i>	37	21	3	3945.8	2967.2	5064.2	37.7
9/17/2012	B2	<i>E. coli</i>	20	2	3	826.1	524.4	1236.7	26.0
9/17/2012	B3	<i>E. coli</i>	8	1	3	293.2	134.7	519.3	26.6
9/17/2012	DPin	Enterococci	8	1	100	8.4	3.9	14.9	22.8
9/17/2012	DPout	Enterococci	4	1	100	5.2	1.9	10.9	33.7
9/17/2012	B1	Enterococci	37	21	100	118.4	89	152	37.7
9/17/2012	B2	Enterococci	20	2	100	24.8	15.8	37.2	26.0
9/17/2012	B3	Enterococci	8	1	100	8.8	4.1	15.7	26.6
9/22/2012	DPin	Coliforms	49	21	3	10826.7	6872.3	16457.8	25.0
9/22/2012	DPout	Coliforms	49	20	3	9785.7	6211.8	14776.8	21.7
9/22/2012	B1	Coliforms	46	14	3	4991.0	3557.9	6812.6	25.7
9/22/2012	B2	Coliforms	46	17	3	5684.5	4163.7	7758.4	28.0
9/22/2012	B3	Coliforms	49	22	3	11899.3	7553.3	17420.6	27.7
9/22/2012	DPin	<i>E. coli</i>	35	1	3	1737.2	1204.5	2415.4	25.0
9/22/2012	DPout	<i>E. coli</i>	4	0	3	117.2	46.9	270.2	21.7
9/22/2012	B1	<i>E. coli</i>	12	2	3	472.0	262.8	768.7	25.7
9/22/2012	B2	<i>E. coli</i>	5	0	3	160.8	70.7	368.6	28.0
9/22/2012	B3	<i>E. coli</i>	5	1	3	192.4	77.2	391.1	27.7
9/22/2012	DPin	Enterococci	1	2	100	2.7	0.6	6.5	25.0
9/22/2012	DPout	Enterococci	2	0	100	1.7	0.3	6.1	21.7
9/22/2012	B1	Enterococci	2	0	100	1.8	0.3	6.4	25.7

9/22/2012	B2	Enterococci	1	5	100	5.6	2.2	11.3	28.0
9/22/2012	B3	Enterococci	1	0	100	0.9	0.1	5.1	27.7
10/3/2012	DPin	Coliforms	49	17	3	8407.2	5501	12889.8	23.1
10/3/2012	DPout	Coliforms	45	7	3	3547.5	2459.7	4884.6	22.6
10/3/2012	B1	Coliforms	45	18	3	5230.3	3831	6924	26.7
10/3/2012	B2	Coliforms	47	15	3	5607.9	3998	7733.6	24.0
10/3/2012	B3	Coliforms	45	18	3	5183.2	3796.4	6861.6	26.0
10/3/2012	DPin	<i>E. coli</i>	12	2	3	456.3	254.1	743	23.1
10/3/2012	DPout	<i>E. coli</i>	6	1	3	211.9	93.1	413.5	22.6
10/3/2012	B1	<i>E. coli</i>	19	1	3	746.1	458.9	1140.7	26.7
10/3/2012	B2	<i>E. coli</i>	11	1	3	390.6	217.6	652.4	24.0
10/3/2012	B3	<i>E. coli</i>	11	0	3	367.3	204.6	642.7	26.0
10/3/2012	DPin	Enterococci	48	2	100	115.4	77.8	167.3	23.1
10/3/2012	DPout	Enterococci	5	1	100	5.4	2.2	11	22.6
10/3/2012	B1	Enterococci	25	9	100	42.5	30.3	58.4	26.7
10/3/2012	B2	Enterococci	10	5	100	14.6	8.5	23.6	24.0
10/3/2012	B3	Enterococci	10	6	100	15.9	9.6	24.8	26.0
10/8/2012	DPin	Coliforms	49	29	3	16486.8	10787.3	24105	21.9
10/8/2012	DPout	Coliforms	42	6	3	3035.7	2164.1	4157.9	27.7
10/8/2012	B1	Coliforms	32	0	3	1489.4	1003.7	2112.4	27.4
10/8/2012	B2	Coliforms	38	2	3	1959.4	1358.7	2735.8	20.0
10/8/2012	B3	Coliforms	47	12	3	5023.4	3483.2	7060.8	23.8
10/8/2012	DPin	<i>E. coli</i>	11	3	3	444.7	247.6	719	21.9
10/8/2012	DPout	<i>E. coli</i>	4	1	3	158.5	54.2	330.6	27.7
10/8/2012	B1	<i>E. coli</i>	6	0	3	193.5	88.8	419.7	27.4
10/8/2012	B2	<i>E. coli</i>	3	0	3	85.0	19.2	248.3	20.0
10/8/2012	B3	<i>E. coli</i>	13	1	3	465.2	267.9	768.7	23.8
10/8/2012	DPin	Enterococci	39	11	100	81.9	60	109	21.9
10/8/2012	DPout	Enterococci	10	4	100	14.3	8	23.2	27.7
10/8/2012	B1	Enterococci	21	1	100	25.6	16.8	38	27.4
10/8/2012	B2	Enterococci	19	2	100	21.6	13.7	32.6	20.0
10/8/2012	B3	Enterococci	23	6	100	33.5	22.6	47.1	23.8
#####	DPin	Coliforms	49	17	3	8578.2	5612.9	13152	24.6
#####	DPout	Coliforms	38	3	3	2099.9	1497.1	2915.3	23.0
#####	B1	Coliforms	41	8	3	2851.3	2088.5	3862.5	23.1
#####	B2	Coliforms	31	2	3	1403.6	973.3	1963.8	21.6
#####	B3	Coliforms	41	8	3	3116.1	2282.4	4221.1	29.6
#####	DPin	<i>E. coli</i>	17	5	3	782.8	496.9	1154.7	24.6
#####	DPout	<i>E. coli</i>	2	0	3	58.3	7.6	205.9	23.0
#####	B1	<i>E. coli</i>	11	1	3	386.0	215	644.8	23.1
#####	B2	<i>E. coli</i>	3	0	3	86.7	19.6	253.3	21.6
#####	B3	<i>E. coli</i>	11	2	3	457.6	246.1	744.4	29.6
#####	DPin	Enterococci	21	1	50	49.3	32.2	73	24.6
#####	DPout	Enterococci	2	2	100	3.6	1.1	7.8	23.0
#####	B1	Enterococci	17	2	100	19.8	12.2	30.4	23.1
#####	B2	Enterococci	6	0	100	5.4	2.5	11.7	21.6
#####	B3	Enterococci	13	2	100	16.2	9.4	26	29.6
#####	DPin	Coliforms	49	43	3	43976.0	28773.5	65379.4	28.6
#####	DPout	Coliforms	49	22	3	12480.1	7922	18271	31.0
#####	B1	Coliforms	49	19	3	10856.7	6891.5	16611.1	33.4
#####	B2	Coliforms	0	1	3	41.0	1.3	151.9	46.3
#####	B3	Coliforms	43	4	3	2753.2	1962.7	3803.9	20.1
#####	DPin	<i>E. coli</i>	37	7	3	2413.2	1720.3	3251.6	28.6
#####	DPout	<i>E. coli</i>	9	3	3	422.1	218.5	701.2	31.0

#####	B1	<i>E. coli</i>	10	1	3	403.9	216.9	703.4	33.4
#####	B2	<i>E. coli</i>	0	1	3	41.0	1.3	151.9	46.3
#####	B3	<i>E. coli</i>	3	1	3	113.8	32.4	252.4	20.1
#####	DPin	Enterococci	36	10	100	74.8	54.8	99.4	28.6
#####	DPout	Enterococci	0	1	100	1.0	0	3.6	31.0
#####	B1	Enterococci	10	0	100	11.0	5.8	20.2	33.4
#####	B2	Enterococci	5	0	100	6.5	2.9	14.8	46.3
#####	B3	Enterococci	0	1	100	0.8	0	3.1	20.1
#####	DPin	Coliforms	49	16	5	4831.4	3255.6	7308.4	24.0
#####	DPout	Coliforms	48	15	5	4142.4	2872.2	5957.2	29.6
#####	B1	Coliforms	49	17	5	5323.5	3483.3	8162	27.1
#####	B2	Coliforms	28	3	5	790.0	547.8	1119.5	25.5
#####	B3	Coliforms	49	17	5	8910.6	5830.4	13661.6	56.5
#####	DPin	<i>E. coli</i>	4	2	5	108.7	41.4	214.7	24.0
#####	DPout	<i>E. coli</i>	5	1	5	118.6	47.6	241.1	29.6
#####	B1	<i>E. coli</i>	12	2	5	288.9	160.9	470.5	27.1
#####	B2	<i>E. coli</i>	9	1	5	195.0	100.9	349	25.5
#####	B3	<i>E. coli</i>	16	2	5	653.3	389.3	998.5	56.5
#####	DPin	Enterococci	7	3	100	9.4	4.5	16.3	24.0
#####	DPout	Enterococci	3	1	100	3.9	1.2	8.7	29.6
#####	B1	Enterococci	5	0	100	4.8	2.2	10.9	27.1
#####	B2	Enterococci	3	2	100	4.6	1.6	9.5	25.5
#####	B3	Enterococci	5	1	100	9.6	3.9	19.5	56.5
11/5/2012	DPin	Coliforms	49	48	5	43498.4	25878.7	#####	25.8
11/5/2012	DPout	Coliforms	49	33	5	16645.4	10891.2	24015.4	41.8
11/5/2012	B1	Coliforms	43	10	5	2059.6	1508.6	2767.5	23.8
11/5/2012	B2	Coliforms	49	39	5	31091.8	20950.7	44844.9	55.1
11/5/2012	B3	Coliforms	49	12	5	4005.0	2620.5	6123.6	25.2
11/5/2012	DPin	<i>E. coli</i>	16	1	5	361.5	222.4	572.5	25.8
11/5/2012	DPout	<i>E. coli</i>	24	4	5	855.0	576.1	1220	41.8
11/5/2012	B1	<i>E. coli</i>	2	0	5	35.3	4.6	124.8	23.8
11/5/2012	B2	<i>E. coli</i>	40	6	5	2622.0	1869.3	3573.3	55.1
11/5/2012	B3	<i>E. coli</i>	7	1	5	151.9	69.7	278.8	25.2
11/5/2012	DPin	Enterococci	27	9	100	46.0	32.9	62.7	25.8
11/5/2012	DPout	Enterococci	8	4	100	14.9	7.7	25	41.8
11/5/2012	B1	Enterococci	4	2	100	5.4	2.1	10.7	23.8
11/5/2012	B2	Enterococci	10	6	100	26.3	15.8	40.9	55.1
11/5/2012	B3	Enterococci	2	0	100	1.8	0.3	6.4	25.2
#####	DPin	Coliforms	49	19	5	5659.1	3592.2	8658.5	23.3
#####	DPout	Coliforms	24	6	5	779.4	525.3	1092.6	31.2
#####	B1	Coliforms	25	2	5	669.6	438.1	966.5	27.5
#####	B2	Coliforms	21	3	5	553.0	350.9	811.5	26.4
#####	B3	Coliforms	20	1	5	455.4	289.2	689.9	23.3
#####	DPin	<i>E. coli</i>	6	0	5	109.9	50.5	238.4	23.3
#####	DPout	<i>E. coli</i>	0	1	5	19.2	0.6	71.2	31.2
#####	B1	<i>E. coli</i>	3	0	5	56.3	12.7	164.5	27.5
#####	B2	<i>E. coli</i>	3	0	5	55.5	12.6	162.1	26.4
#####	B3	<i>E. coli</i>	2	0	5	35.1	4.6	123.9	23.3
#####	DPin	Enterococci	14	0	100	14.0	8.1	23.3	23.3
#####	DPout	Enterococci	3	2	100	4.9	1.7	10.3	31.2
#####	B1	Enterococci	1	0	100	0.9	0.1	5.1	27.5
#####	B2	Enterococci	1	1	100	1.8	0.3	5.4	26.4
#####	B3	Enterococci	3	0	100	2.7	0.7	7.8	23.3
#####	DPin	Coliforms	49	43	10	6234.2	4079.1	9268.5	24.4

#####	DPout	Coliforms	49	44	10	7832.2	5124.6	11866.2	33.9
#####	B1	Coliforms	45	12	10	619.7	441.9	840	22.6
#####	B2	Coliforms	49	32	10	2988.1	1955.2	4240.3	23.4
#####	B3	Coliforms	49	11	10	936.0	612.5	1402.1	23.7
#####	DPin	<i>E. coli</i>	40	8	10	411.5	293.4	553.2	24.4
#####	DPout	<i>E. coli</i>	25	7	10	220.4	152.9	306.1	33.9
#####	B1	<i>E. coli</i>	11	0	10	52.7	29.4	92.2	22.6
#####	B2	<i>E. coli</i>	18	1	10	100.4	61.8	155.4	23.4
#####	B3	<i>E. coli</i>	7	2	10	41.9	19.3	74	23.7
#####	DPin	Enterococci	48	15	100	96.4	67	138.7	24.4
#####	DPout	Enterococci	19	5	100	15.0	9.9	21.9	33.9
#####	B1	Enterococci	6	2	100	3.6	1.6	6.6	22.6
#####	B2	Enterococci	7	0	100	3.3	1.6	6.5	23.4
#####	B3	Enterococci	5	3	100	3.7	1.7	6.7	23.7
#####	DPin	Coliforms	49	25	20	2059.5	1307.3	3072.3	25.4
#####	DPout	Coliforms	49	47	20	12031.7	8107.4	23451.6	33.0
#####	B1	Coliforms	43	7	20	487.1	347.2	663.6	26.0
#####	B2	Coliforms	46	10	20	628.4	448	861.3	22.2
#####	B3	Coliforms	49	18	20	1320.7	838.4	2023.4	22.4
#####	DPin	<i>E. coli</i>	24	2	20	154.2	103.9	223.9	25.4
#####	DPout	<i>E. coli</i>	25	4	20	195.5	131.8	278	33.0
#####	B1	<i>E. coli</i>	5	1	20	28.2	11.4	57.5	26.0
#####	B2	<i>E. coli</i>	4	1	20	22.1	7.6	46.1	22.2
#####	B3	<i>E. coli</i>	11	1	20	57.4	32	95.9	22.4
#####	DPin	Enterococci	47	12	100	153.9	106.8	216.4	25.4
#####	DPout	Enterococci	7	1	100	8.5	3.9	15.6	33.0
#####	B1	Enterococci	1	0	100	0.9	0.1	5	26.0
#####	B2	Enterococci	0	1	100	0.9	0	3.2	22.2
#####	B3	Enterococci	1	1	100	1.7	0.3	5.1	22.4
12/3/2012	DPin	Coliforms	49	14	20	1083.4	708.9	1624.1	23.7
12/3/2012	DPout	Coliforms	49	29	20	2904.5	1900.4	4246.6	33.5
12/3/2012	B1	Coliforms	36	5	20	297.9	212.4	407.3	22.0
12/3/2012	B2	Coliforms	49	31	20	3363.5	2200.8	4880.6	35.7
12/3/2012	B3	Coliforms	49	22	20	1954.2	1240.5	2861	33.9
12/3/2012	DPin	<i>E. coli</i>	19	0	20	101.9	62.8	157.8	23.7
12/3/2012	DPout	<i>E. coli</i>	15	0	20	87.7	50.6	143.2	33.5
12/3/2012	B1	<i>E. coli</i>	6	2	20	36.1	16	65.6	22.0
12/3/2012	B2	<i>E. coli</i>	25	1	20	181.3	118.7	265.4	35.7
12/3/2012	B3	<i>E. coli</i>	19	2	20	130.7	83	197.3	33.9
12/3/2012	DPin	Enterococci	26	6	100	38.7	26.9	54	23.7
12/3/2012	DPout	Enterococci	7	2	100	9.6	4.5	17	33.5
12/3/2012	B1	Enterococci	5	0	100	4.4	2	10.2	22.0
12/3/2012	B2	Enterococci	4	0	100	4.3	1.8	9.9	35.7
12/3/2012	B3	Enterococci	1	0	100	1.0	0.2	5.6	33.9
#####	DPin	Coliforms	47	7	20	620.4	430.2	876.2	22.1
#####	DPout	Coliforms	49	18	20	2026.4	1286.3	3104.4	49.4
#####	B1	Coliforms	40	6	20	381.7	272.1	520.1	22.9
#####	B2	Coliforms	48	15	20	1067.4	740.2	1535.1	31.7
#####	B3	Coliforms	25	2	20	154.5	101.1	223	21.4
#####	DPin	<i>E. coli</i>	21	1	20	119.2	78	176.6	22.1
#####	DPout	<i>E. coli</i>	10	1	20	79.8	42.9	139	49.4
#####	B1	<i>E. coli</i>	6	0	20	27.3	12.6	59.4	22.9
#####	B2	<i>E. coli</i>	5	0	20	25.5	11.3	58.3	31.7
#####	B3	<i>E. coli</i>	0	1	20	4.2	0.2	15.7	21.4

#####	DPin	Enterococci	10	4	100	13.3	7.4	21.5	22.1
#####	DPout	Enterococci	0	2	100	2.6	0.4	7.4	49.4
#####	B1	Enterococci	6	0	100	5.4	2.6	11.9	22.9
#####	B2	Enterococci	4	0	100	4.0	1.7	9.3	31.7
#####	B3	Enterococci	0	1	100	0.8	0	3.2	21.4
#####	DPin	Coliforms	49	31	20	2771.6	1813.5	4021.7	22.0
#####	DPout	Coliforms	43	14	20	616.6	451.6	816.5	28.8
#####	B1	Coliforms	47	13	20	869.2	602.7	1219.4	31.5
#####	B2	Coliforms	41	5	20	477.1	340.2	653	36.7
#####	B3	Coliforms	39	6	20	371.1	264.7	505.3	24.9
#####	DPin	<i>E. coli</i>	28	7	20	215.4	149.4	295.2	22.0
#####	DPout	<i>E. coli</i>	9	1	20	51.0	26.5	91.3	28.8
#####	B1	<i>E. coli</i>	19	4	20	138.7	88.1	203.6	31.5
#####	B2	<i>E. coli</i>	11	1	20	70.3	39.2	117.5	36.7
#####	B3	<i>E. coli</i>	6	0	20	28.1	12.9	60.9	24.9
#####	DPin	Enterococci	0	3	100	2.6	0.6	6.3	22.0
#####	DPout	Enterococci	0	1	100	0.9	0	3.5	28.8
#####	B1	Enterococci	3	1	100	4.0	1.2	8.9	31.5
#####	B2	Enterococci	1	0	100	1.1	0.2	5.8	36.7
#####	B3	Enterococci	1	0	100	0.9	0.1	4.9	24.9
#####	DPin	Coliforms	48	18	50	411.1	285.1	578.5	19.3
#####	DPout	Coliforms	49	40	50	2068.1	1393.6	2980.7	27.8
#####	B1	Coliforms	48	11	50	310.1	209.1	448.2	20.0
#####	B2	Coliforms	49	43	50	3120.5	2041.8	4639.3	39.6
#####	B3	Coliforms	49	33	50	1261.1	825.1	1819.4	23.1
#####	DPin	<i>E. coli</i>	32	1	50	83.2	56.1	117.1	19.3
#####	DPout	<i>E. coli</i>	28	3	50	81.4	56.6	115.5	27.8
#####	B1	<i>E. coli</i>	11	2	50	24.2	13.1	39.3	20.0
#####	B2	<i>E. coli</i>	38	3	50	160.6	114.5	222.9	39.6
#####	B3	<i>E. coli</i>	19	4	50	49.3	31.4	72.6	23.1
#####	DPin	Enterococci	49	47	100	1998.0	1346.4	3894.4	19.3
#####	DPout	Enterococci	48	21	100	263.3	182.6	368.3	27.8
#####	B1	Enterococci	38	11	100	75.9	55.6	100.9	20.0
#####	B2	Enterococci	33	4	100	64.3	44.8	89	39.6
#####	B3	Enterococci	32	4	100	48.2	33.4	67	23.1
1/7/2013	DPin	Coliforms	49	16	50	500.9	337.6	757.8	26.7
1/7/2013	DPout	Coliforms	48	22	50	595.8	413.2	844.2	33.2
1/7/2013	B1	Coliforms	31	4	50	92.5	64.2	128.9	23.8
1/7/2013	B2	Coliforms	47	9	50	294.7	204.4	415.2	29.8
1/7/2013	B3	Coliforms	49	24	50	742.3	471.3	1108.9	21.8
1/7/2013	DPin	<i>E. coli</i>	27	2	50	73.5	49.6	104.4	26.7
1/7/2013	DPout	<i>E. coli</i>	14	1	50	34.5	20.6	56.2	33.2
1/7/2013	B1	<i>E. coli</i>	3	0	50	5.3	1.3	15.7	23.8
1/7/2013	B2	<i>E. coli</i>	6	0	50	12.0	5.6	26.1	29.8
1/7/2013	B3	<i>E. coli</i>	15	2	50	33.9	20.3	52.8	21.8
1/7/2013	DPin	Enterococci	28	6	100	44.4	30.9	61.4	26.7
1/7/2013	DPout	Enterococci	3	2	100	5.1	1.7	10.6	33.2
1/7/2013	B1	Enterococci	1	1	100	1.7	0.3	5.2	23.8
1/7/2013	B2	Enterococci	0	1	100	0.9	0	3.6	29.8
1/7/2013	B3	Enterococci	1	2	100	2.6	0.6	6.3	21.8
1/14/2013	DPin	Coliforms	49	36	50	1473.6	993	2118.1	21.6
1/14/2013	DPout	Coliforms	46	13	50	295.8	210.9	403.8	27.2
1/14/2013	B1	Coliforms	38	6	50	136.8	97.5	185.7	22.6
1/14/2013	B2	Coliforms	49	16	50	501.4	337.9	758.5	26.7

1/14/2013	B3	Coliforms	49	18	50	553.2	351.2	847.6	25.9
1/14/2013	DPin	<i>E. coli</i>	49	25	50	784.2	497.8	1169.9	21.6
1/14/2013	DPout	<i>E. coli</i>	8	0	50	15.7	8.2	30.9	27.2
1/14/2013	B1	<i>E. coli</i>	5	1	50	10.8	4.4	22	22.6
1/14/2013	B2	<i>E. coli</i>	11	0	50	22.3	12.4	39	26.7
1/14/2013	B3	<i>E. coli</i>	10	0	50	19.8	10.3	36.2	25.9
1/14/2013	DPin	Enterococci	39	13	100	85.9	63	113.7	21.6
1/14/2013	DPout	Enterococci	0	1	100	0.9	0	3.4	27.2
1/14/2013	B1	Enterococci	2	0	100	1.7	0.3	6.2	22.6
1/14/2013	B2	Enterococci	1	2	100	2.7	0.6	6.7	26.7
1/14/2013	B3	Enterococci	2	2	100	3.7	1.1	8.1	25.9
1/20/2013	DPin	Coliforms	49	42	50	2349.1	1537.1	3428.1	26.2
1/20/2013	DPout	Coliforms	49	40	50	2130.0	1435.3	3070	29.9
1/20/2013	B1	Coliforms	45	16	50	294.7	215.9	391.4	26.5
1/20/2013	B2	Coliforms	49	45	50	3462.3	2333	5413.5	33.3
1/20/2013	B3	Coliforms	49	26	50	883.3	560.7	1304.7	26.3
1/20/2013	DPin	<i>E. coli</i>	49	32	50	1241.1	812.2	1761.3	26.2
1/20/2013	DPout	<i>E. coli</i>	43	17	50	272.0	204.6	356.1	29.9
1/20/2013	B1	<i>E. coli</i>	19	6	50	56.4	38.1	81.5	26.5
1/20/2013	B2	<i>E. coli</i>	46	17	50	368.0	269.6	502.2	33.3
1/20/2013	B3	<i>E. coli</i>	39	6	50	151.2	107.8	205.9	26.3
1/20/2013	DPin	Enterococci	48	18	100	224.9	156	316.5	26.2
1/20/2013	DPout	Enterococci	28	5	100	45.0	31.2	62.7	29.9
1/20/2013	B1	Enterococci	11	0	100	11.1	6.2	19.5	26.5
1/20/2013	B2	Enterococci	28	6	100	48.8	33.9	67.5	33.3
1/20/2013	B3	Enterococci	24	3	100	32.5	21.9	47	26.3
1/27/2013	DPin	Coliforms	48	14	50	352.3	244.4	505.7	20.6
1/27/2013	DPout	Coliforms	49	15	50	497.4	325.5	758.6	30.0
1/27/2013	B1	Coliforms	46	12	50	277.7	198	382.2	24.9
1/27/2013	B2	Coliforms	41	8	50	169.3	124	229.4	22.3
1/27/2013	B3	Coliforms	35	5	50	116.1	82.9	158.3	23.9
1/27/2013	DPin	<i>E. coli</i>	14	1	50	29.1	17.3	47.3	20.6
1/27/2013	DPout	<i>E. coli</i>	13	3	50	34.8	20.1	54.9	30.0
1/27/2013	B1	<i>E. coli</i>	7	2	50	17.0	7.9	30.1	24.9
1/27/2013	B2	<i>E. coli</i>	3	1	50	7.0	2	15.6	22.3
1/27/2013	B3	<i>E. coli</i>	10	0	50	19.3	10	35.3	23.9
1/27/2013	DPin	Enterococci	26	3	100	33.5	22.6	47.5	20.6
1/27/2013	DPout	Enterococci	14	3	100	18.8	11.2	29.3	30.0
1/27/2013	B1	Enterococci	1	3	100	3.5	1	7.9	24.9
1/27/2013	B2	Enterococci	2	1	100	2.6	0.7	6.4	22.3
1/27/2013	B3	Enterococci	1	0	100	0.9	0.1	4.9	23.9

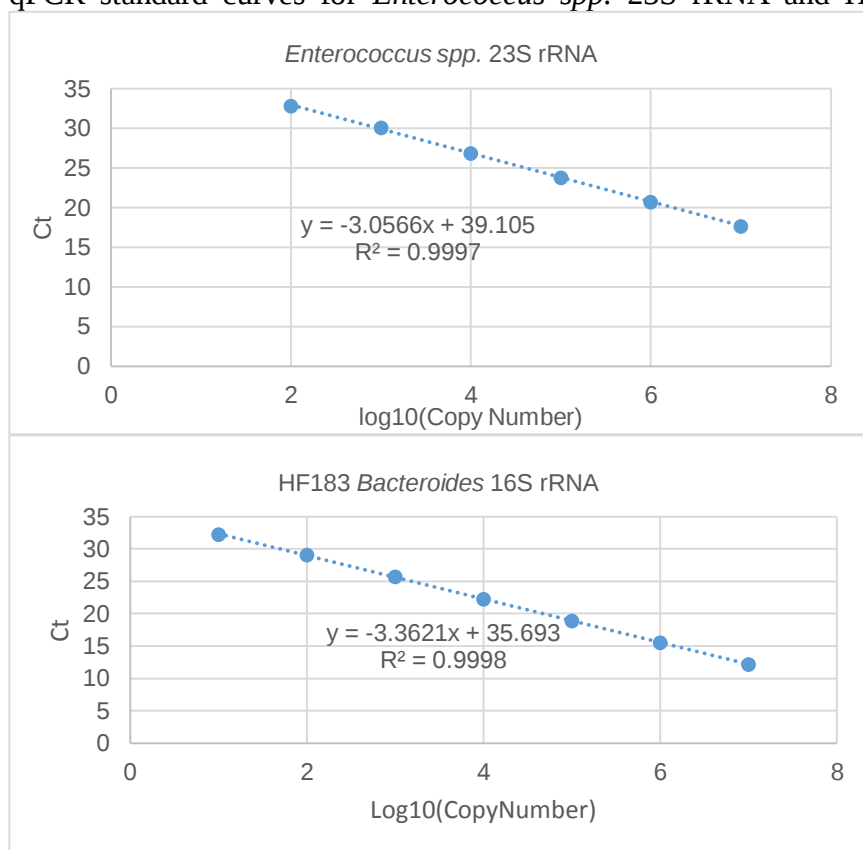
Appendix B: Intrastorm FIB monitoring data

Data for intrastorm sampling from the sampling bridge 1 of the StREAM Lab: sampling and subsequent measurements of FIB (*E. coli* and Enterococci) concentrations via culture-based methods by 2013 NSF-REU students (Romnia Benitez, Richard Sawyer, Erin Schaberg, and Emily von Wagoner).

Storm #1 (6/26/2013)

Date Time	SampleID	MPN/100mL		CN/100mL	
		<i>E. coli</i>	Enterococci	<i>Enterococcus spp.</i>	HF183
6/26/2013 13:37	1	13327	8420	197586.3	7588
6/26/2013 13:52	2	20459	10497	258348.7	1828
6/26/2013 14:07	3	19559	24809	526935.5	3104
6/26/2013 14:22	4	18600	6695	195641.1	6400.8
6/26/2013 14:37	5	7800	3692	138472.3	4059.2
6/26/2013 14:52	6	6631	1336	70000	4802
6/26/2013 15:07	7	8162	2462	30641.1	3040
6/26/2013 15:22	8	5833	1579	29843.8	2200
6/26/2013 15:37	9	5653	2847	34186.1	5752
6/26/2013 15:52	10	6294	512	50555.6	3576
6/26/2013 16:07	11	6828	1089	42790.7	4696
6/26/2013 16:22	12	8088	516	43077	4704
6/26/2013 16:37	13	7894	571	51621.7	4392
6/26/2013 16:52	14	3170	626	60810.9	5488
6/26/2013 17:07	15	3451	1712	45618	4168
6/26/2013 17:22	16	2751	979	45232.6	4704
6/26/2013 17:37	17	1731	1449	149777.8	9590
6/26/2013 17:52	18	1890	1731	151754.4	9184
6/26/2013 18:07	19	2718	632	65545.5	3232
6/26/2013 18:22	20	2086	979	68089.9	4120
6/26/2013 18:37	21	2751	738	45116.3	2536
6/26/2013 18:52	22	2433	306	42687.5	2042
6/26/2013 19:07	23	1596	632	40258.7	1548

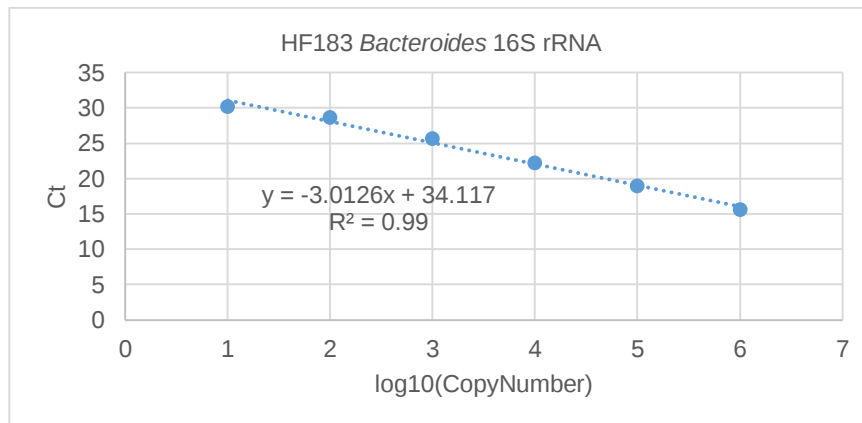
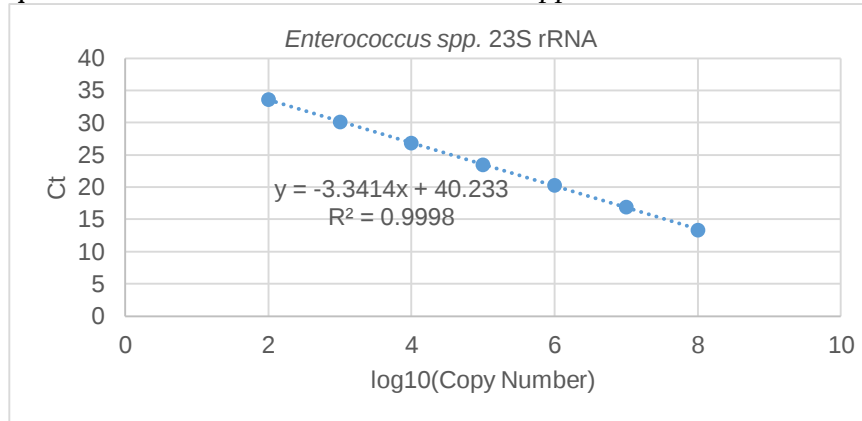
qPCR standard curves for *Enterococcus* spp. 23S rRNA and HF183 *Bacteroides* 16S rRNA



Storm #2 (6/27/2013)

Date Time	SampleID	MPN/100mL		CN/100mL	
		<i>E. coli</i>	Enterococci	<i>Enterococcus spp.</i>	HF183
6/27/2013 10:00	6	8859	4434	11389	1035.5
6/27/2013 10:15	7	4954	2785	12478.3	1741.9
6/27/2013 10:30	8	30759	13735	10801	1244
6/27/2013 10:45	9	30759	13735	8993.3	923.3
6/27/2013 11:00	10	22468	11455	7151	902.4
6/27/2013 11:15	11	21426	6871	51993.4	1968.8
6/27/2013 11:30	12	18501	9854	172873.2	3437.8
6/27/2013 11:45	13	9063	3966	41160.2	1312.3
6/27/2013 12:00	14	10193	3544	165093.5	1449.4
6/27/2013 12:15	15	8197	4969	112372.6	1982.8
6/27/2013 12:30	16	7712	3545	23649.3	1438.4
6/27/2013 12:45	17	11528	2405	127319.1	2124
6/27/2013 13:00	18	13169	7227	47968	1741.2
6/27/2013 13:15	19	15386	8014	96007.2	2382
6/27/2013 13:30	20	16162	5043	105226.7	2512.9
6/27/2013 13:45	21	9075	9075	89722	2474.8
6/27/2013 14:00	22	11370	8392	40716.9	2456
6/27/2013 14:15	23	11776	8624	55519.9	2905.7

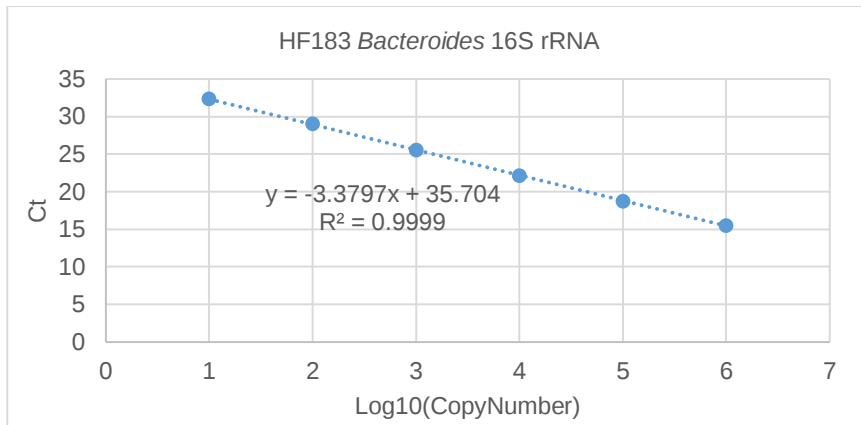
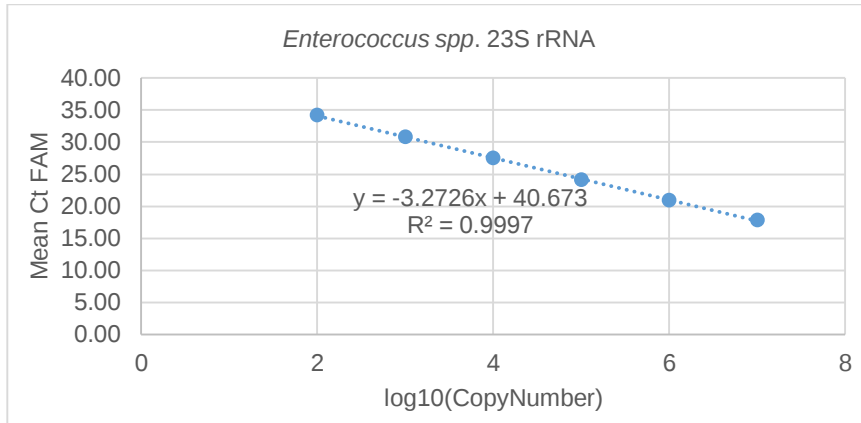
qPCR standard curves for *Enterococcus spp.* 23S rRNA and HF183 *Bacteroides* 16S rRNA



Storm #3 (6/30/2013)

Date Time	SampleID	MPN/100mL		CN/100mL	
		<i>E. coli</i>	Enterococci	<i>Enterococcus spp.</i>	HF183
6/30/2013 18:45	1	12498	2624	510800	2552
6/30/2013 19:00	2	36540	7430	947440	4784
6/30/2013 19:15	3	23593	12669	1267360	8640
6/30/2013 19:30	4	13344	5850	541360	6192
6/30/2013 19:45	5	12591	7279	723120	4904
6/30/2013 20:00	6	17853	7634	781440	3808
6/30/2013 20:15	7	12007	7000	562480	4104
6/30/2013 20:30	8	17216	6049	464240	3144
6/30/2013 20:45	9	20635	8709	470640	2784
6/30/2013 21:00	10	15967	6116	353200	2856
6/30/2013 21:15	11	17890	4638	285520	2392
6/30/2013 21:30	12	15286	8907	316800	2168
6/30/2013 21:45	13	12112	1458	549760	2944
6/30/2013 22:00	14	11190	8668	381680	3232
6/30/2013 22:15	15	13169	7976	384160	4160
6/30/2013 22:30	16	14209	14695	663920	2840
6/30/2013 22:45	17	19890	3129	607200	2776
6/30/2013 23:00	18	17890	2405	671280	2696
6/30/2013 23:15	19	16640	4890	706000	2560
6/30/2013 23:30	20	12740	4307.5	429200	2920
6/30/2013 23:45	21	10758	3725	419680	2632
7/1/2013 0:00	22	13135	3877	410160	2192
7/1/2013 0:15	23	8574	4284	265760	4336
7/1/2013 0:30	24	12356	4585	297840	2128

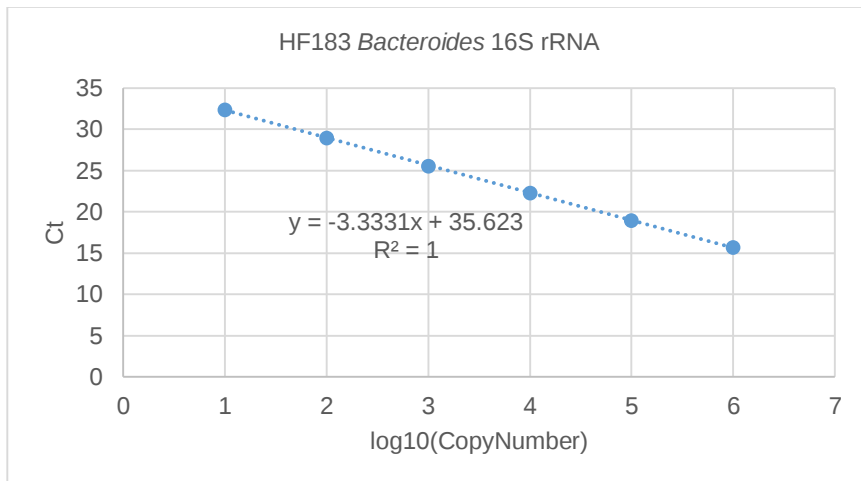
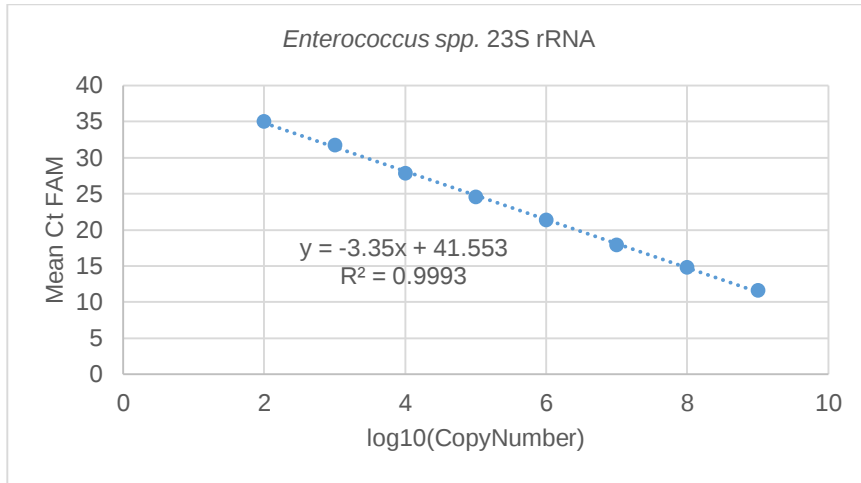
qPCR standard curves for *Enterococcus* spp. 23S rRNA and HF183 *Bacteroides* 16S rRNA



Storm #4 (7/2/2013)

Date Time	SampleID	MPN/100mL		CN/100mL	
		<i>E. coli</i>	Enterococci	<i>Enterococcus spp.</i>	HF183
7/2/2013 8:47	1	1068	3442.5	7603.8	2761.1
7/2/2013 9:17	2	2954	2300	44483.1	46469.3
7/2/2013 9:47	3	2992	3405	117243.8	83788.4
7/2/2013 10:17	4	2378	5121	3877	3170.2
7/2/2013 10:47	5	5371	3684	84295.9	141644.5
7/2/2013 11:17	6	3839	2718	89060.9	94229.6
7/2/2013 11:47	7	2751	1336	124725.6	102374
7/2/2013 12:17	8	1596	409	119686.5	152827.7
7/2/2013 12:47	9	3319	516	149130.8	84369.2
7/2/2013 13:17	10	3361	512	52461	98898.3
7/2/2013 13:47	11	2992	521	33100.7	94882.8
7/2/2013 14:17	12	2307	516	63594.3	167187.8
7/2/2013 14:47	13	1989	202	37718.4	103798.3
7/2/2013 15:17	14	2182	852	37460	110456.7
7/2/2013 15:47	15	1989	306	19231.6	3350.4
7/2/2013 16:17	16	1613	413	60191.9	9574.6
7/2/2013 16:47	17	969	304	21615.4	5586.1
7/2/2013 17:17	18	836	306	74999.8	9574.6
7/2/2013 17:47	19	1350	1199	62296.4	4603.6
7/2/2013 18:17	20	13327	9831	62296.4	4541.3
7/2/2013 18:47	21	5475	6408	200412.9	4479
7/2/2013 19:17	22	8014	4223	72965.9	4416.7
7/2/2013 19:47	23	13540	5948	734690.9	2388.3
7/2/2013 20:17	24	15152	7478	1073	5036.2

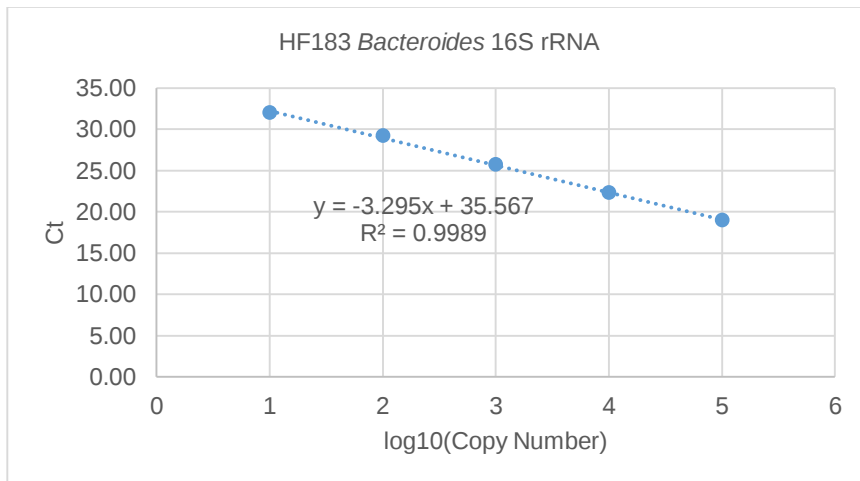
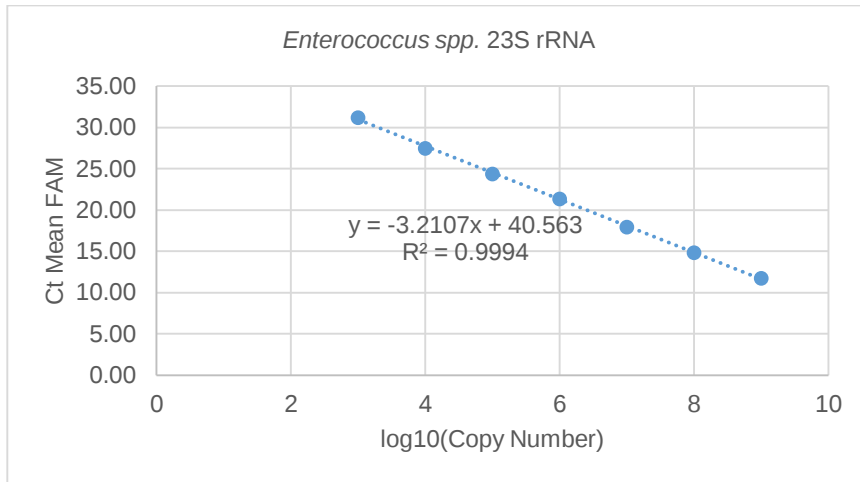
qPCR standard curves for *Enterococcus* spp. 23S rRNA and HF183 *Bacteroides* 16S rRNA



Storm #5 (7/10/2013)

Date Time	SampleID	MPN/100mL		CN/100mL	
		<i>E. coli</i>	Enterococci	<i>Enterococcus spp.</i>	HF183
7/10/2013 16:00	6	306	3839.5	27493.1	462.2
7/10/2013 16:30	7	100	201	15346.6	567.4
7/10/2013 17:00	8	11528	24890	668441.3	10708.1
7/10/2013 17:30	9	43517	21426	804297	4756.3
7/10/2013 18:00	10	16162	10758	420572.2	3829.9
7/10/2013 18:30	11	7478	11264	360429.2	4826.9
7/10/2013 19:00	12	13344	24890	718376.6	6473.5
7/10/2013 19:30	13	13327	14497	375587.6	6657
7/10/2013 20:00	14	8296	9895	319451.6	6428.4
7/10/2013 20:30	15	11874	11528	1099563.9	7496.7
7/10/2013 21:00	16	16695	8329	1029799	13865.6
7/10/2013 21:30	17	13344	13135	991445.7	8621.2
7/10/2013 22:00	18	10497	8624	791913.4	6942
7/10/2013 22:30	19	8624	7712	509598.1	6428.4
7/10/2013 23:00	20	8361	6844	663307.6	3102.4
7/10/2013 23:30	21	4959	6053	487458.8	4734.3
7/11/2013 0:00	22	6367	4479	858243.5	3893
7/11/2013 0:30	23	6504	2281	485394.4	5137.6
7/11/2013 1:00	24	3405	2133	369102.4	5821.5

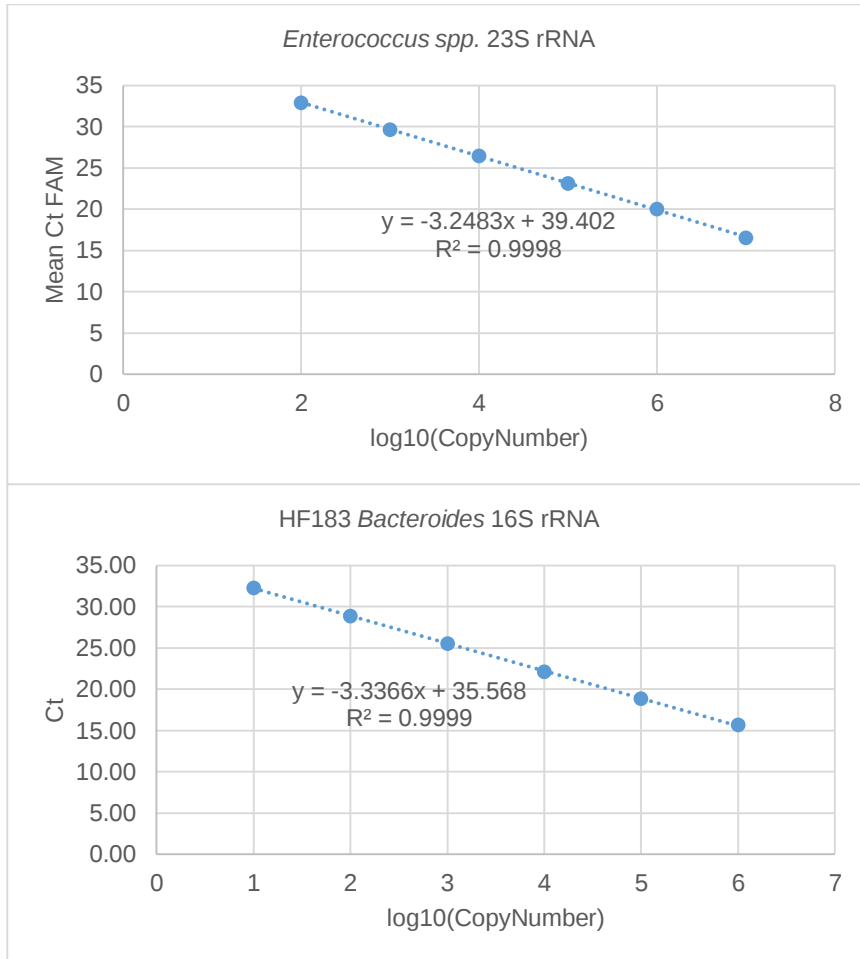
qPCR standard curves for *Enterococcus* spp. 23S rRNA and HF183 *Bacteroides* 16S rRNA



Storm #6 (7/21/2013)

Date Time	SampleID	MPN/100mL		CN/100mL	
		<i>E. coli</i>	Enterococci	<i>Enterococcus spp.</i>	HF183
7/21/2013 11:55	3	100	201	4080	157.9
7/21/2013 12:10	4	202	202	3800	188.8
7/21/2013 12:25	5	512	1118	14460	339.3
7/21/2013 12:40	6	3545	2034	84280	12512.6
7/21/2013 12:55	7	5291	6945	120760	12233.6
7/21/2013 13:10	8	8574	13914	253400	8251.2
7/21/2013 13:25	9	5392	4808	62240	6009.8
7/21/2013 13:40	10	4434	2621	72800	4558
7/21/2013 13:55	11	3267	2011	50240	3466.5
7/21/2013 14:10	12	1350	1849	36280	3161.8
7/21/2013 14:25	13	1849	951	56120	3295.4
7/21/2013 14:40	14	1869	1323	63280	3482.5
7/21/2013 14:55	15	2230	1310	57600	2500.5
7/21/2013 15:10	16	1712	626	57440	3434.8
7/21/2013 15:25	17	1946	860	33640	2642.5
7/21/2013 15:40	18	2334	1089	44200	2831.3
7/21/2013 15:55	19	1336	626	39720	2735.2
7/21/2013 16:10	20	1596	306	30120	2005.1
7/21/2013 16:25	21	1563	516	42920	1047.4
7/21/2013 16:40	22	1749	951	38000	1438.7
7/21/2013 16:55	23	1890	745	23660	969.2
7/21/2013 17:10	24	1677	516	40500	892.1

qPCR standard curves for *Enterococcus* spp. 23S rRNA and HF183 *Bacteroides* 16S rRNA



Appendix C: HSPF model

HSPF UCI file under “free-phase” scenario:

***Simulated fecal coliform concentrations were converted to *E. coli* concentrations via: $E. coli = 0.98814866 * (\text{Fecal coliform}^{0.91905})$.

RUN

GLOBAL

UCI Stroubles Creek Watershed-"free-phase" scenario

START 2008/01/01 00:00 END 2013/12/31 24:00

RUN INTERP OUTPT LEVELS 1 0

RESUME 0 RUN 1 UNITS 1

END GLOBAL

FILES

<FILE> <UN#>***<----FILE NAME----->
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	91	N22_sed.out
	44	..\Cattle.mut
	45	..\Wildlife.mut
	46	..\Straight_Pipes.mut
	60	..\N22_Spills.mut
WDM2	26	..\..\N22_MET1.wdm
WDM3	27	..\..\N22_MET2.wdm
	55	FreeFC.OUT

END FILES

OPN SEQUENCE

INGRP INDELT 01:00

MUTSIN	1
MUTSIN	2
MUTSIN	3
MUTSIN	20
PERLND	101
PERLND	201
PERLND	301
PERLND	401
PERLND	102
PERLND	202
PERLND	302
PERLND	402
PERLND	103
PERLND	203
PERLND	303
PERLND	403
PERLND	104
PERLND	204
PERLND	304
PERLND	404
PERLND	105
PERLND	205

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PERLND      305
PERLND      405
PERLND      106
PERLND      206
PERLND      306
PERLND      406
PERLND      407
PERLND      607
PERLND      108
PERLND      308
PERLND      408
PERLND      109
PERLND      309
PERLND      409
IMPLND      101
RCHRES       9
RCHRES       8
RCHRES       7
RCHRES       6
RCHRES       5
RCHRES       4
RCHRES       3
RCHRES       2
RCHRES       1
PLTGEN      13

END INGRP
END OPN SEQUENCE

PERLND
ACTIVITY
*** <PLS > Active Sections ***
*** x - x ATMP SNOW PWAT SED PST PWG PQAL MSTL PEST NITR PHOS TRAC ***
101 607 0 0 1 0 0 0 1 0 0 0 0 0
END ACTIVITY

PRINT-INFO
*** < PLS> Print-flags
PIVL PYR
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101 607 4 4 4 4 4 4 4 4 4 4 4 4
1 12
END PRINT-INFO

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*** x - x in out
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201 Cropland-1 1 1 0 0 0 0
301 Pasture-1 1 1 0 0 0 0
401 Residential-1 1 1 0 0 0 0
102 Forest-2 1 1 0 0 0 0
202 Cropland-2 1 1 0 0 0 0
302 Pasture-2 1 1 0 0 0 0

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201	0.	12.0	0.268	141.8	0.118	0.1
0.990						
202	0.	12.0	0.297	122.5	0.147	0.1
0.990						
203	0.	12.0	0.274	184.1	0.124	0.1
0.990						
204	0.	12.0	0.32	206.4	0.17	0.1
0.990						
205	0.	12.0	0.312	198.2	0.162	0.1
0.990						
206	0.	12.0	0.252	247.3	0.102	0.1
0.990						
301	0.	12.0	0.267	123.9	0.117	0.1
0.990						
302	0.	12.0	0.301	130.6	0.151	0.1
0.990						
303	0.	12.0	0.286	111.1	0.136	0.1
0.990						
304	0.	12.0	0.316	145.1	0.166	0.1
0.990						
305	0.	12.0	0.307	143.7	0.157	0.1
0.990						
306	0.	12.0	0.329	125.9	0.179	0.1
0.990						
308	0.	12.0	0.222	176.8	0.072	0.1
0.990						
309	0.	12.0	0.276	148.3	0.126	0.1
0.990						
401	0.	10.0	0.254	137.5	0.124	0.1
0.966						
402	0.	10.0	0.26	132.5	0.13	0.1
0.966						
403	0.	10.0	0.256	139.4	0.126	0.1
0.966						
404	0.	10.0	0.255	156.7	0.125	0.1
0.966						
405	0.	10.0	0.248	146.2	0.118	0.1
0.966						
406	0.	10.0	0.234	147.6	0.104	0.1
0.966						
407	0.	10.0	0.209	143.6	0.079	0.1
0.966						
408	0.	10.0	0.204	153.2	0.074	0.1
0.966						
409	0.	10.0	0.221	151.0	0.091	0.1
0.966						
607	0.	10.0	0.500	143	0.100	0.1
0.966						

END PWAT-PARM2

PWAT-PARM3

*** < PLS>	PETMAX	PETMIN	INFEXP	INFILD	DEEPFR	BASETP
AGWETP						
*** x - x	(deg F)	(deg F)				

101 607 40. 35. 2. 2. 0.29 0.030
 0.00
 END PWAT-PARM3

PWAT-PARM4
 *** <PLS > CEPSC UZSN NSUR INTFW IRC LZETP
 *** x - x (in) (in) (1/day)
 101 109 0.20 1.00 0.50 5.0 0.90 0.6
 201 206 0.10 1.00 0.35 5.0 0.90 0.4
 301 309 0.10 1.00 0.35 5.0 0.90 0.3
 401 409 0.05 1.00 0.20 5.0 0.90 0.2
 607 0.00 1.00 0.35 5.0 0.90 0.2
 END PWAT-PARM4

PWAT-STATE1
 *** < PLS> PWATER state variables (in)
 *** x - x CEPS SURS UZS IFWS LZS AGWS
 GWVS
 101 607 0.0 0.00 0.9 0.00 9.4 1
 0.00
 END PWAT-STATE1

MON-INTERCEP
 *** <PLS > Interception storage capacity at start of each month (in)
 *** x - x JAN FEB MAR APR MAY JUN JUL AUG SEP OCT NOV DEC
 101 109 0.20 0.20 0.20 0.20 0.20 0.20 0.20 0.20 0.20 0.20 0.20 0.20
 201 206 0.20 0.20 0.20 0.20 0.20 0.22 0.22 0.22 0.20 0.20 0.20 0.20
 301 309 0.15 0.15 0.15 0.15 0.15 0.16 0.16 0.16 0.16 0.16 0.16 0.16
 401 409 0.05 0.05 0.05 0.05 0.05 0.05 0.05 0.05 0.05 0.05 0.05 0.05
 607 0.01 0.01 0.01 0.01 0.01 0.01 0.01 0.01 0.01 0.01 0.01 0.01
 END MON-INTERCEP

MON-UZSN
 *** <PLS > Upper zone storage at start of each month (inches)
 *** x - x JAN FEB MAR APR MAY JUN JUL AUG SEP OCT NOV DEC
 101 109 1.10 1.10 1.10 1.00 1.00 1.00 1.00 1.00 1.00 1.10 1.10 1.10
 201 206 1.10 1.10 1.10 1.00 1.00 1.00 1.00 1.00 1.00 1.10 1.10 1.10
 301 309 1.10 1.10 1.10 1.00 1.00 1.00 1.00 1.00 1.00 1.10 1.10 1.10
 401 409 1.10 1.10 1.10 1.00 1.00 1.00 1.00 1.00 1.00 1.10 1.10 1.10
 607 1.10 1.10 1.10 1.00 1.00 1.00 1.00 1.00 1.00 1.10 1.10 1.10
 END MON-UZSN

MON-LZETPARM
 *** <PLS > Lower zone evapotransp parm at start of each month
 *** x - x JAN FEB MAR APR MAY JUN JUL AUG SEP OCT NOV DEC
 101 109 0.65 0.65 0.65 0.65 0.65 0.66 0.66 0.66 0.65 0.65 0.65 0.65
 201 206 0.40 0.40 0.40 0.40 0.40 0.40 0.40 0.40 0.40 0.40 0.40 0.40
 301 309 0.40 0.40 0.40 0.40 0.40 0.40 0.40 0.40 0.40 0.40 0.40 0.40
 401 409 0.20 0.20 0.20 0.20 0.20 0.20 0.20 0.20 0.20 0.20 0.20 0.20
 607 0.20 0.20 0.20 0.20 0.20 0.20 0.20 0.20 0.20 0.20 0.20 0.20
 END MON-LZETPARM

NQUALS
 # # NQAL ***

1 9 1
END NQUALS

QUAL-PROPS

*** <PLS > Identifiers and Flags
*** x - x QUALID QTID QSD VPFW VPFS QSO VQO QIFW VIQC QAGW
VAQC
101 634FC # 0 0 0 1 1 1 0 1
0
END QUAL-PROPS

QUAL-INPUT

*** Storage on surface and nonseasonal parameters
*** SQO POTFW POTFS ACQOP SQOLIM WSQOP IOQC AOQC
*** <PLS > qty/ac qty/ton qty/ton qty/ qty/ ac.day
*** x - x
*** Forest
101 109 0E+10 0. 0. 1E+10 9E+10 2.00 177. 118.
*** Cropland
201 203 0E+10 0. 0. 1E+10 9E+10 0.20 531. 354.
204 206 0E+10 0. 0. 1E+10 9E+10 0.10 531. 354.
*** Pasture
301 303 0E+10 0. 0. 1E+10 9E+10 0.20 177. 118.
304 309 0E+10 0. 0. 1E+10 9E+10 0.10 177. 118.
*** Residential
401 403 0E+10 0. 0. 1E+10 9E+10 0.10 531. 354.
404 409 0E+10 0. 0. 1E+10 9E+10 0.01 531. 354.
*** Water
607 0E+10 0. 0. 1E+10 9E+10 0.10 531. 354.
END QUAL-INPUT

MON-POTFW

JAN FEB MAR APR MAY JUN JUL AUG SEP OCT NOV DEC

101 109 .030 .010 .180 .060 .120 .302 .201 .804 .400 .120 .240 .015
201 209 2.55 0.43 0.50 1.59 3.17 4.75 3.17 2.66 3.17 3.17 2.66 1.28
301 309 2.55 0.43 0.50 1.59 3.17 4.75 3.17 2.66 3.17 3.17 2.66 1.28
401 409 .21 .28 .48 1.28 2.57 1.93 2.57 5.14 0.28 1.24 1.24 .42
607
END MON-POTFW

MON-ACCUM

*** <PLS > Value at start of each month for accum rate of QUALOF
(#/ac.day)
*** x - x JAN FEB MAR APR MAY JUN JUL AUG SEP OCT NOV DEC
*** N22-1
201 12E0612E0611E0712E0711E0712E0612E0612E0612E0630E0631E0612E06
301 15E0716E0717E0717E0717E0717E0718E0718E0718E0714E0714E0714E07
401 53E0753E0753E0753E0753E0753E0753E0753E0753E0753E0753E07
101 12E0612E0612E0612E0612E0612E0612E0612E0612E0612E0612E06
*** N22-2
202 60E0560E0589E0592E0591E0560E0560E0560E0560E0566E0565E0560E05
302 60E0560E0580E0582E0581E0560E0560E0560E0582E0581E0580E0560E05
402 68E0768E0768E0768E0768E0768E0768E0768E0768E0768E0768E07


```

404      42E0842E0842E0842E0842E0842E0842E0842E0842E0842E0842E0842E08
104      30E0730E0730E0730E0730E0730E0730E0730E0730E0730E0730E0730E07
*** N22-5
205      18E0718E0710E0910E0910E0918E0718E0718E0718E0720E0820E0818E07
305      75E0984E0988E0990E0991E0993E0995E0997E0999E0970E0972E0973E09
405      10E0910E0910E0910E0910E0910E0910E0910E0910E0910E0910E0910E09
105      20E0720E0720E0720E0720E0720E0720E0720E0720E0720E0720E0720E07
*** N22-6
206      41E0741E0776E0879E0876E0841E0741E0741E0741E0717E0818E0841E07
306      99E1011E1111E1112E1112E1112E1112E1112E1113E1113E1189E1093E1096E10
406      12E0812E0812E0812E0812E0812E0812E0812E0812E0812E0812E0812E08
106      41E0741E0741E0741E0741E0741E0741E0741E0741E0741E0741E0741E07
*** N22-7
407      53E0853E0853E0853E0853E0853E0853E0853E0853E0853E0853E0853E08
*** N22-8
308      38E0738E0740E0740E0740E0738E0738E0738E0740E0740E0740E0738E07
408      16E0916E0916E0916E0916E0916E0916E0916E0916E0916E0916E0916E09
108      41E0741E0741E0741E0741E0741E0741E0741E0741E0741E0741E0741E07
*** N22-9
309      59E0759E0761E0761E0761E0759E0759E0759E0761E0761E0761E0759E07
409      29E0929E0929E0929E0929E0929E0929E0929E0929E0929E0929E0929E09
109      11E0811E0811E0811E0811E0811E0811E0811E0811E0811E0811E0811E08
END MON-SQOLIM
END PERLND

```

IMPLND

```

ACTIVITY
*** <ILS >           Active Sections
*** x - x ATMP SNOW IWAT  SLD  IWG IQAL
101          0      0      1      0      0      1
END ACTIVITY

```

```

PRINT-INFO
*** <ILS > ***** Print-flags ***** PIVL  PYR
*** x - x ATMP SNOW IWAT  SLD  IWG IQAL *****
101          4      4      4      4      4      4      1      9
END PRINT-INFO

```

```

GEN-INFO
***          Name          Unit-systems  Printer BinaryOut
*** <ILS >          t-series Engl Metr Engl Metr
*** x - x          in  out
101          1      1      0      0      0      0
END GEN-INFO

```

```

IWAT-PARM1
*** <ILS >          Flags
*** x - x CSNO RTOP  VRS  VNN RTLI
101          0      1      0      0      0
END IWAT-PARM1

```

```

IWAT-PARM2
*** <ILS >          LSUR          SLSUR          NSUR          RETSC
*** x - x          (ft)          (in)

```

```

101 106      100.      0.150      0.10      0.150
107      100.      0.150      0.10      0.300
108 109      100.      0.150      0.10      0.250
END IWAT-PARM2

IWAT-PARM3
*** <ILS >      PETMAX      PETMIN
*** x - x      (deg F)      (deg F)
101      40.      35.
END IWAT-PARM3

IWAT-STATE1
*** <ILS > IWATER state variables (inches)
*** x - x      RETS      SURS
101      0.0      0.00
END IWAT-STATE1

QUAL-PROPS
*** <ILS >
*** x - x      QUALID      QTID      QSD      VPFW      QSO      VQO
101      FC      #      0      0      1      0
END QUAL-PROPS

QUAL-INPUT
***      SQO      POTFW      ACQOP      SQOLIM      WSQOP
*** <ILS > qty/ac qty/ton      qty/      qty/ac      in/hr
*** x - x      ac.day
101      1E+07      0.      1E+07      3E+07      0.01
END QUAL-INPUT

END IMPLND

RCHRES
ACTIVITY
*** RCHRES Active sections
*** x - x HYFG ADFG CNFG HTFG SDFG GQFG OXFG NUFG PKFG PHFG
1 9 1 1 0 0 1 1 0 0 0 0
END ACTIVITY

PRINT-INFO
*** RCHRES Printout level flags
*** x - x HYDR ADCA CONS HEAT SED GQL OXRX NUTR PLNK PHCB PIVL PYR
1 9 4 4 4 4 4 4 4 4 4 1 9
END PRINT-INFO

GEN-INFO
***      Name      Nexits      Unit Systems      Printer
*** RCHRES      t-series      Engl Metr LKFG
*** x - x      in out
1 9 StroublesCrk      1      1 1 0 0 0 0
0
END GEN-INFO

HYDR-PARM1

```

```

***          Flags for HYDR section
***RC HRES  VC A1 A2 A3  ODFVFG for each *** ODGTFG for each      FUNCT
for each
*** x  -  x  FG FG FG FG  possible  exit *** possible  exit      possible
exit
1      9      0  1  1  1      4  0  0  0  0      0  0  0  0  0      1  1  1
1  1

```

END HYDR-PARM1

HYDR-PARM2

```

*** RCHRES FTBW FTBU      LEN      DELTH      STCOR      KS      DB50
*** x  -  x      (miles)      (ft)      (ft)      (in)
1      0.      1      2.29      119.7      3.2      0.5      0.2
2      0.      2      2.41      62.91      3.2      0.5      0.2
3      0.      3      0.49      6.7      3.2      0.5      0.2
4      0.      4      0.54      7.17      3.2      0.5      0.2
5      0.      5      0.80      16.28      3.2      0.5      0.2
6      0.      6      0.62      17.07      3.2      0.5      0.2
7      0.      7      0.28      7.87      3.2      0.5      0.2
8      0.      8      1.30      90.65      3.2      0.5      0.2
9      0.      9      1.78      173.9      3.2      0.5      0.2

```

END HYDR-PARM2

MON-CONVF

```

*** RCHRES  Monthly f(VOL) adjustment factors
*** x  -  x  JAN  FEB  MAR  APR  MAY  JUN  JUL  AUG  SEP  OCT  NOV  DEC
1      9  0.90  0.89  0.89  0.91  0.93  1.99  1.99  1.99  0.99  0.98  0.98  0.90
END MON-CONVF

```

HYDR-INIT

```

***          Initial conditions for HYDR section
*** RCHRES      VOL  CAT Initial value of COLIND      initial value of
OUTDGT
*** x  -  x      ac-ft      for each possible  exit  for each possible
exit,ft3
1      9      10.0      4.2  4.5  4.5  4.5  4.2      2.1  1.2  0.5
1.2  1.8

```

END HYDR-INIT

GQ-QALDATA

```

*** RCHRES      GQID      DQAL      CONCID      CONV      QTYID
*** x  -  x      concid
1      9FC      100.      #/10      0.0035  #

```

END GQ-QALDATA

GQ-QALFG

```

*** RCHRES HDRL OXID PHOT VOLT BIOD  GEN SDAS
*** x  -  x
1      9      0      0      0      0      0      1      0

```

END GQ-QALFG

GQ-GENDECAY

```

*** RCHRES      FSTDEC      THFST
*** x  -  x      (/day)

```

1	3	1.15	1.05	
7		4.00	1.05	
4	6	1.15	1.05	
8	9	1.15	1.05	

END GQ-GENDECAY
END RCHRES

FTABLES

FTABLE 1

rows	cols				***
4	4				
depth	area	volume	outflow1		***
0.	5.22	0.	0.		
0.01	5.22	0.05	0.		
2.93	11.55	24.61	476.35		
45.59	601.48	1773.82	169167.		

END FTABLE 1

FTABLE 2

rows	cols				***
4	4				
depth	area	volume	outflow1		***
0.	19.43	0.	0.		
0.01	19.43	0.19	0.		
1.9	19.2	36.68	252.84		
83.92	437.52	25063.55	1006730.09		

END FTABLE 2

FTABLE 3

rows	cols				***
4	4				
depth	area	volume	outflow1		***
0.	3.38	0.	0.		
0.01	3.38	0.03	0.		
1.76	3.34	5.9	203.87		
28.	47.32	853.68	64940.09		

END FTABLE 3

FTABLE 4

rows	cols				***
4	4				
depth	area	volume	outflow1		***
0.	3.59	0.	0.		
0.01	3.59	0.04	0.		
1.66	3.54	5.92	174.8		
25.28	71.51	901.73	44353.9		

END FTABLE 4

FTABLE 5

rows	cols				***
4	4				
depth	area	volume	outflow1		***
0.	5.12	0.	0.		
0.01	5.12	0.05	0.		

1.63	5.05	8.3	166.84
11.48	95.09	569.86	13866.32

END FTABLE 5

FTABLE 6

rows	cols			***
4	4			
depth	area	volume	outflow1	***
0.	3.38	0.	0.	
0.01	3.38	0.03	0.	
1.44	3.32	4.83	118.21	
11.61	143.71	940.84	22476.73	

END FTABLE 6

FTABLE 7

rows	cols			***
7	4			
depth	area	volume	outflow1	***
0.	0.00	0.	0.	
1.46	1.82	2.2568	0.405	
2.92	3.82	6.2568	0.567	
6.84	4.64	8.9544	2.066	
9.84	7.28	9.5630	2000	
14.84	7.30	34.383	6000	
31.01	338.78	3848.03	30707.05	

END FTABLE 7

FTABLE 8

rows	cols			***
4	4			
depth	area	volume	outflow1	***
0.	2.51	0.	0.	
0.01	2.51	0.03	0.	
1.16	2.46	2.89	65.36	
25.77	186.12	2992.61	295449.88	

END FTABLE 8

FTABLE 9

rows	cols			***
4	4			
depth	area	volume	outflow1	***
0.	5.43	0.	0.	
0.01	5.43	0.05	0.	
1.01	5.31	5.43	44.58	
11.84	132.28	848.34	19856.96	

END FTABLE 9

END FTABLES

NETWORK

MUTSIN	01	OUTPUT	01	1	SAME	RCHRES	01	INFLOW	IDQAL
MUTSIN	01	OUTPUT	02	1	SAME	RCHRES	02	INFLOW	IDQAL
MUTSIN	01	OUTPUT	03	1	SAME	RCHRES	03	INFLOW	IDQAL
MUTSIN	01	OUTPUT	04	1	SAME	RCHRES	04	INFLOW	IDQAL
MUTSIN	01	OUTPUT	05	1	SAME	RCHRES	05	INFLOW	IDQAL

```

MUTSIN 01 OUTPUT      06      1      SAME RCHRES 06      INFLOW IDQAL
MUTSIN 01 OUTPUT      07      1      SAME RCHRES 07      INFLOW IDQAL
MUTSIN 01 OUTPUT      08      1      SAME RCHRES 08      INFLOW IDQAL
MUTSIN 01 OUTPUT      09      1      SAME RCHRES 09      INFLOW IDQAL
*** Wildlife          1
MUTSIN 02 OUTPUT      01      1      SAME RCHRES 01      INFLOW IDQAL
MUTSIN 02 OUTPUT      02      1      SAME RCHRES 02      INFLOW IDQAL
MUTSIN 02 OUTPUT      03      1      SAME RCHRES 03      INFLOW IDQAL
MUTSIN 02 OUTPUT      04      1      SAME RCHRES 04      INFLOW IDQAL
MUTSIN 02 OUTPUT      05      1      SAME RCHRES 05      INFLOW IDQAL
MUTSIN 02 OUTPUT      06      1      SAME RCHRES 06      INFLOW IDQAL
MUTSIN 02 OUTPUT      07      1      SAME RCHRES 07      INFLOW IDQAL
MUTSIN 02 OUTPUT      08      1      SAME RCHRES 08      INFLOW IDQAL
MUTSIN 02 OUTPUT      09      1      SAME RCHRES 09      INFLOW IDQAL
*** Straight Pipes    1
MUTSIN 03 OUTPUT      01      1      SAME RCHRES 01      INFLOW IDQAL
MUTSIN 03 OUTPUT      02      1      SAME RCHRES 02      INFLOW IDQAL
MUTSIN 03 OUTPUT      03      1      SAME RCHRES 03      INFLOW IDQAL
MUTSIN 03 OUTPUT      04      1      SAME RCHRES 04      INFLOW IDQAL
MUTSIN 03 OUTPUT      05      1      SAME RCHRES 05      INFLOW IDQAL
MUTSIN 03 OUTPUT      06      1      SAME RCHRES 06      INFLOW IDQAL
MUTSIN 03 OUTPUT      07      1      SAME RCHRES 07      INFLOW IDQAL
MUTSIN 03 OUTPUT      08      1      SAME RCHRES 08      INFLOW IDQAL
MUTSIN 03 OUTPUT      09      1      SAME RCHRES 09      INFLOW IDQAL
*** PreP Spills into Reaches
MUTSIN 20 OUTPUT      01      1      SAME RCHRES 05      INFLOW IVOL
MUTSIN 20 OUTPUT      02      1      SAME RCHRES 05      INFLOW IDQAL
MUTSIN 20 OUTPUT      03      1      SAME RCHRES 07      INFLOW IVOL
MUTSIN 20 OUTPUT      04      1      SAME RCHRES 07      INFLOW IDQAL
MUTSIN 20 OUTPUT      05      1      SAME RCHRES 08      INFLOW IVOL
MUTSIN 20 OUTPUT      06      1      SAME RCHRES 08      INFLOW IDQAL
MUTSIN 20 OUTPUT      07      1      SAME RCHRES 09      INFLOW IVOL
MUTSIN 20 OUTPUT      08      1      SAME RCHRES 09      INFLOW IDQAL
RCHRES 9 GQUAL DQAL          PLTGEN 13      INPUT MEAN 1
RCHRES 8 GQUAL DQAL          PLTGEN 13      INPUT MEAN 2
RCHRES 7 GQUAL DQAL          PLTGEN 13      INPUT MEAN 3
RCHRES 6 GQUAL DQAL          PLTGEN 13      INPUT MEAN 4
RCHRES 5 GQUAL DQAL          PLTGEN 13      INPUT MEAN 5
RCHRES 4 GQUAL DQAL          PLTGEN 13      INPUT MEAN 6
RCHRES 3 GQUAL DQAL          PLTGEN 13      INPUT MEAN 7
RCHRES 2 GQUAL DQAL          PLTGEN 13      INPUT MEAN 8
RCHRES 1 GQUAL DQAL          PLTGEN 13      INPUT MEAN 9
END NETWORK

```

```

MUTSIN
MUTSINFO
<-range><mfl><npt><nmn><nli><mis> ***
# - # MFL NPT NMN NLI MSFG ***
01      44      0      09      25      2
02      45      0      09      25      2
03      46      0      09      25      2
20      60      0      08      25      2
END MUTSINFO
END MUTSIN

```

```

PLTGEN
PLOTINFO
  # - # FILE  NPT  NMN LABL  PYR PIVL
  13      55    0    9    0   12    1
END PLOTINFO

GEN-LABELS
  # - #<-----Title----->    ***    <-----Y axis-
----->
  13      FC concen. in free-phase                                #/100mL
END GEN-LABELS

SCALING
  # - #          YMIN      YMAX      IVLIN      THRESH ***
  13          0.      1.E+10      100.
END SCALING

CURV-DATA      (First curve)
  # - #          <-Curve label--> Line Intg  Col Tran ***
                        type  eqv  code  code ***
  13          subwatershed 9                                AVER
END CURV-DATA

CURV-DATA      (Second curve)
  # - #          <-Curve label--> Line Intg  Col Tran ***
                        type  eqv  code  code ***
  13          subwatershed 8                                AVER
END CURV-DATA

CURV-DATA      (Third curve)
  # - #          <-Curve label--> Line Intg  Col Tran ***
                        type  eqv  code  code ***
  13          subwatershed 7                                AVER
END CURV-DATA

CURV-DATA      (Fourth curve)
  # - #          <-Curve label--> Line Intg  Col Tran ***
                        type  eqv  code  code ***
  13          subwatershed 6                                AVER
END CURV-DATA

CURV-DATA      (Fifth curve)
  # - #          <-Curve label--> Line Intg  Col Tran ***
                        type  eqv  code  code ***
  13          subwatershed 5                                AVER
END CURV-DATA

CURV-DATA      (Sixth curve)
  # - #          <-Curve label--> Line Intg  Col Tran ***
                        type  eqv  code  code ***
  13          subwatershed 4                                AVER
END CURV-DATA

```

```

CURV-DATA
      <-Curve label--> Line Intg  Col Tran ***
      # - #           type  eqv code code ***
      13             subwatershed 3          AVER
END CURV-DATA

CURV-DATA
      <-Curve label--> Line Intg  Col Tran ***
      # - #           type  eqv code code ***
      13             subwatershed 2          AVER
END CURV-DATA

CURV-DATA
      <-Curve label--> Line Intg  Col Tran ***
      # - #           type  eqv code code ***
      13             subwatershed 1          AVER
END CURV-DATA
END PLTGEN

EXT SOURCES
<-Volume-> <Member> SsysSgap<--Mult-->Tran <-Target vols> <-Grp> <-
Member-> ***
<Name>      x <Name> x tem strg<-factor->strg <Name>      x      x      <Name> x
x ***
WDM3      11 PREC      ENGLZERO      SAME PERLND 101 607 EXTNL PREC
WDM2      13 ATEM      ENGL      SAME PERLND 101 607 EXTNL GATMP
WDM2      17 DEWP      ENGL      SAME PERLND 101 607 EXTNL DTMPG
WDM2      14 WIND      ENGL      SAME PERLND 101 607 EXTNL WINMOV
WDM2      15 SOLR      ENGL      SAME PERLND 101 607 EXTNL SOLRAD
WDM2      16 PEVT      ENGL      SAME PERLND 101 607 EXTNL PETINP
WDM3      11 PREC      ENGLZERO      SAME IMPLND 101      EXTNL PREC
WDM2      13 ATEM      ENGL      SAME IMPLND 101      EXTNL GATMP
WDM2      17 DEWP      ENGL      SAME IMPLND 101      EXTNL DTMPG
WDM2      14 WIND      ENGL      SAME IMPLND 101      EXTNL WINMOV
WDM2      15 SOLR      ENGL      SAME IMPLND 101      EXTNL SOLRAD
WDM2      16 PEVT      ENGL      SAME IMPLND 101      EXTNL PETINP
WDM3      11 PREC      ENGLZERO      SAME RCHRES 1 9 EXTNL PREC
WDM2      13 ATEM      ENGL      SAME RCHRES 1 9 EXTNL GATMP
WDM2      17 DEWP      ENGL      SAME RCHRES 1 9 EXTNL DEWTMP
WDM2      14 WIND      ENGL      SAME RCHRES 1 9 EXTNL WIND
WDM2      15 SOLR      ENGL      SAME RCHRES 1 9 EXTNL SOLRAD
WDM2      18 CLOU      ENGL      SAME RCHRES 1 9 EXTNL CLOUD
WDM2      12 EVAP      ENGL      SAME RCHRES 1 9 EXTNL POTEV
END EXT SOURCES

SCHEMATIC
<-Volume->      <--Area-->      <-Volume->      <ML#> ***
<sb>
<Name>      x      <-factor->      <Name>      x      ***      x
x
PERLND 101      806.55      RCHRES 1 2
PERLND 201      113.73      RCHRES 1 2
PERLND 301      447.2      RCHRES 1 2
PERLND 401      266.02      RCHRES 1 2

```

PERLND 102	1136.15	RCHRES	2	2
PERLND 202	29.37	RCHRES	2	2
PERLND 302	125.28	RCHRES	2	2
PERLND 402	95.67	RCHRES	2	2
PERLND 103	280.88	RCHRES	3	2
PERLND 203	39.29	RCHRES	3	2
PERLND 303	325.81	RCHRES	3	2
PERLND 403	247.12	RCHRES	3	2
PERLND 104	10.95	RCHRES	4	2
PERLND 204	35.7	RCHRES	4	2
PERLND 304	95.92	RCHRES	4	2
PERLND 404	51.4	RCHRES	4	2
PERLND 105	50.5	RCHRES	5	2
PERLND 205	23.72	RCHRES	5	2
PERLND 305	290.17	RCHRES	5	2
PERLND 405	534.23	RCHRES	5	2
PERLND 106	3.54	RCHRES	6	2
PERLND 206	33.63	RCHRES	6	2
PERLND 306	24.01	RCHRES	6	2
PERLND 406	197.27	RCHRES	6	2
PERLND 407	139.63	RCHRES	7	2
PERLND 607	6.86	RCHRES	7	2
PERLND 108	57.21	RCHRES	8	2
PERLND 308	77.28	RCHRES	8	2
PERLND 408	698.21	RCHRES	8	2
PERLND 109	3.71	RCHRES	9	2
PERLND 309	6.37	RCHRES	9	2
PERLND 409	491.81	RCHRES	9	2
IMPLND 101	98.63	RCHRES	1	1
IMPLND 101	27.88	RCHRES	2	1
IMPLND 101	78.69	RCHRES	3	1
IMPLND 101	18.77	RCHRES	4	1
IMPLND 101	351.80	RCHRES	5	1
IMPLND 101	72.96	RCHRES	6	1
IMPLND 101	51.64	RCHRES	7	1
IMPLND 101	258.24	RCHRES	8	1
IMPLND 101	181.90	RCHRES	9	1

*** Reach Connections ***

*** Reach 2 => Reach 1				
RCHRES 2		RCHRES	1	3
*** Reach 3 => Reach 2				
RCHRES 3		RCHRES	2	3
*** Reach 4 => Reach 3				
RCHRES 4		RCHRES	3	3
*** Reach 05 => Reach 4				
RCHRES 5		RCHRES	4	3
*** Reach 06 => Reach 5				
RCHRES 6		RCHRES	5	3
*** Reach 07 => Reach 6				
RCHRES 7		RCHRES	6	3
*** Reach 08 => Reach 7				
RCHRES 8		RCHRES	7	3

*** Reach 09 => Reach 7
RCHRES 9
END SCHEMATIC

RCHRES 7 3

MASS-LINK

MASS-LINK 2
<-Volume-> <-Grp> <-Member-><--Mult-->
Member-> ***
<Name> <Name> x x<-factor->
x ***
PERLND PWATER PERO 0.0833333
PERLND PQUAL POQUAL 1 1.00
END MASS-LINK 2

<-Target vols> <-Grp> <-
<Name> <Name> x
RCHRES INFLOW IVOL
RCHRES INFLOW IDQAL 1

MASS-LINK 3
<-Volume-> <-Grp> <-Member-><--Mult-->
Member-> ***
<Name> <Name> x x<-factor->
x ***
RCHRES ROFLOW
END MASS-LINK 3

<-Target vols> <-Grp> <-
<Name> <Name> x
RCHRES INFLOW

MASS-LINK 4
<-Volume-> <-Grp> <-Member-><--Mult-->
Member-> ***
<Name> <Name> x x<-factor->
x ***
RCHRES ROFLOW ROVOL
RCHRES HYDR RO
END MASS-LINK 4

<-Target vols> <-Grp> <-
<Name> <Name> x
COPY INPUT MEAN 1
COPY INPUT MEAN 2

MASS-LINK 5
<-Volume-> <-Grp> <-Member-><--Mult-->
Member-> ***
<Name> <Name> x x<-factor->
x ***
RCHRES OFLOW 1
END MASS-LINK 5

<-Target vols> <-Grp> <-
<Name> <Name> x
RCHRES INFLOW

MASS-LINK 6
<-Volume-> <-Grp> <-Member-><--Mult-->
Member-> ***
<Name> <Name> x x<-factor->
x ***
RCHRES OFLOW 2
END MASS-LINK 6
END MASS-LINK

<-Target vols> <-Grp> <-
<Name> <Name> x
RCHRES INFLOW

END RUN

HSPF UCI file under “sediment-attached” scenario:

***Simulated fecal coliform concentrations were converted to *E. coli* concentrations via: $E. coli = 0.98814866 * (\text{Fecal coliform}^{0.91905})$.

RUN

GLOBAL

UCI Stroubles Creek Hydrology Calibration

START 2008/01/01 00:00 END 2013/12/31 24:00

RUN INTERP OUTPT LEVELS 1 0

RESUME 0 RUN 1 UNITS 1

END GLOBAL

FILES

<FILE> <UN#>***<----FILE NAME----->
----->

MESSU	24	N22_sed.ech
	91	N22_sed.out
	44	..\Cattle.mut
	45	..\Wildlife.mut
	46	..\Straight_Pipes.mut
	60	..\N22_Spills.mut
WDM2	26	..\..\N22_MET1.wdm
WDM3	27	..\..\N22_MET2.wdm
	31	SedStorage.OUT
	32	BedDepth.OUT
	33	ShearStress.OUT
	34	TSS.OUT
	37	Inflows.OUT
	35	Outflow.OUT
	36	DepScour.OUT
	38	Flow.OUT
	51	SusSiltFC.OUT
	52	SusClayFC.OUT
	53	BedSiltFC.OUT
	54	BedClayFC.OUT
	55	FreeFC.OUT
	56	DSQAL.OUT

END FILES

OPN SEQUENCE

INGRP INDELT 01:00

MUTSIN	1
MUTSIN	2
MUTSIN	3
MUTSIN	20
PERLND	101
PERLND	201
PERLND	301
PERLND	401
PERLND	102
PERLND	202
PERLND	302
PERLND	402
PERLND	103

PERLND	203
PERLND	303
PERLND	403
PERLND	104
PERLND	204
PERLND	304
PERLND	404
PERLND	105
PERLND	205
PERLND	305
PERLND	405
PERLND	106
PERLND	206
PERLND	306
PERLND	406
PERLND	407
PERLND	607
PERLND	108
PERLND	308
PERLND	408
PERLND	109
PERLND	309
PERLND	409
IMPLND	101
RCHRES	9
RCHRES	8
RCHRES	7
RCHRES	6
RCHRES	5
RCHRES	4
RCHRES	3
RCHRES	2
RCHRES	1
PLTGEN	1
PLTGEN	2
PLTGEN	3
PLTGEN	4
PLTGEN	5
PLTGEN	6
PLTGEN	7
PLTGEN	8
PLTGEN	9
PLTGEN	10
PLTGEN	11
PLTGEN	12
PLTGEN	13
PLTGEN	14

END INGRP
END OPN SEQUENCE

PERLND
ACTIVITY

*** <PLS >	Active Sections	***
*** x -	x ATMP SNOW PWAT SED PST PWG PQAL MSTL PEST NITR PHOS TRAC	***

```

101 607 0 0 1 1 0 0 1 0 0 0 0 0
END ACTIVITY

```

```

PRINT-INFO
*** < PLS>                                Print-flags
PIVL  PYR
*** x  - x ATMP SNOW PWAT  SED  PST  PWG PQAL MSTL PEST NITR PHOS TRAC
101 607 4 4 4 4 4 4 4 4 4 4 4 4
1 12
END PRINT-INFO

```

```

GEN-INFO
***                                     Name      Unit-systems  Printer BinaryOut
*** <PLS >                             t-series  Engl Metr Engl Metr
*** x  - x                             in  out
101  Forest -1                          1    1    0    0    0    0
201  Cropland-1                         1    1    0    0    0    0
301  Pasture-1                          1    1    0    0    0    0
401  Residential-1                      1    1    0    0    0    0
102  Forest-2                          1    1    0    0    0    0
202  Cropland-2                         1    1    0    0    0    0
302  Pasture-2                          1    1    0    0    0    0
402  Residential-2                      1    1    0    0    0    0
103  Forest-3                          1    1    0    0    0    0
203  Cropland-3                         1    1    0    0    0    0
303  Pasture-3                          1    1    0    0    0    0
403  Residential-3                      1    1    0    0    0    0
104  Forest-4                          1    1    0    0    0    0
204  Cropland-4                         1    1    0    0    0    0
304  Pasture-4                          1    1    0    0    0    0
404  Residential-4                      1    1    0    0    0    0
105  Forest-5                          1    1    0    0    0    0
205  Cropland-5                         1    1    0    0    0    0
305  Pasture-5                          1    1    0    0    0    0
405  Residential-5                      1    1    0    0    0    0
106  Forest-6                          1    1    0    0    0    0
206  Cropland-6                         1    1    0    0    0    0
306  Pasture-6                          1    1    0    0    0    0
406  Residential-6                      1    1    0    0    0    0
407  Residential-7                      1    1    0    0    0    0
607  Water-7                           1    1    0    0    0    0
108  Forest-8                          1    1    0    0    0    0
308  Pasture-8                          1    1    0    0    0    0
408  Residential-8                      1    1    0    0    0    0
109  Forest-9                          1    1    0    0    0    0
309  Pasture-9                          1    1    0    0    0    0
409  Residential-9                      1    1    0    0    0    0
END GEN-INFO

```

```

PWAT-PARM1
*** <PLS >                                Flags
*** x  - x CSNO RTOP UZFG  VCS  VUZ  VNN VIFW VIRC  VLE  IFFC  HWT  IRRG
101 607 0 1 1 1 1 0 0 0 1 0 0 0
END PWAT-PARM1

```

PWAT-PARM2 *** < PLS> AGWRC *** x - x (1/day)	FOREST	LZSN (in)	INFILT (in/hr)	LSUR (ft)	SLSUR	KVARY (1/in)
101	1.	15.0	0.357	124.2	0.107	0.1
0.990						
102	1.	15.0	0.358	132.6	0.108	0.1
0.990						
103	1.	15.0	0.373	133.1	0.123	0.1
0.990						
104	1.	15.0	0.36	238.1	0.11	0.1
0.990						
105	1.	15.0	0.368	164.3	0.118	0.1
0.990						
106	1.	15.0	0.342	121.1	0.092	0.1
0.990						
108	1.	15.0	0.318	189.9	0.068	0.1
0.990						
109	1.	15.0	0.337	234.3	0.087	0.1
0.990						
201	0.	12.0	0.268	141.8	0.118	0.1
0.990						
202	0.	12.0	0.297	122.5	0.147	0.1
0.990						
203	0.	12.0	0.274	184.1	0.124	0.1
0.990						
204	0.	12.0	0.32	206.4	0.17	0.1
0.990						
205	0.	12.0	0.312	198.2	0.162	0.1
0.990						
206	0.	12.0	0.252	247.3	0.102	0.1
0.990						
301	0.	12.0	0.267	123.9	0.117	0.1
0.990						
302	0.	12.0	0.301	130.6	0.151	0.1
0.990						
303	0.	12.0	0.286	111.1	0.136	0.1
0.990						
304	0.	12.0	0.316	145.1	0.166	0.1
0.990						
305	0.	12.0	0.307	143.7	0.157	0.1
0.990						
306	0.	12.0	0.329	125.9	0.179	0.1
0.990						
308	0.	12.0	0.222	176.8	0.072	0.1
0.990						
309	0.	12.0	0.276	148.3	0.126	0.1
0.990						
401	0.	10.0	0.254	137.5	0.124	0.1
0.966						
402	0.	10.0	0.26	132.5	0.13	0.1
0.966						

403	0.	10.0	0.256	139.4	0.126	0.1
0.966						
404	0.	10.0	0.255	156.7	0.125	0.1
0.966						
405	0.	10.0	0.248	146.2	0.118	0.1
0.966						
406	0.	10.0	0.234	147.6	0.104	0.1
0.966						
407	0.	10.0	0.209	143.6	0.079	0.1
0.966						
408	0.	10.0	0.204	153.2	0.074	0.1
0.966						
409	0.	10.0	0.221	151.0	0.091	0.1
0.966						
607	0.	10.0	0.500	143	0.100	0.1
0.966						

END PWAT-PARM2

PWAT-PARM3

*** < PLS>	PETMAX	PETMIN	INFEXP	INFILD	DEEPFR	BASETP
AGWETP						
*** x - x (deg F)	(deg F)					
101 607	40.	35.	2.	2.	0.29	0.030

0.00

END PWAT-PARM3

PWAT-PARM4

*** <PLS >	CEPSC	UZSN	NSUR	INTFW	IRC	LZETP
*** x - x (in)	(in)				(1/day)	
101 109	0.20	1.00	0.50	5.0	0.90	0.6
201 206	0.10	1.00	0.35	5.0	0.90	0.4
301 309	0.10	1.00	0.35	5.0	0.90	0.3
401 409	0.05	1.00	0.20	5.0	0.90	0.2
607	0.00	1.00	0.35	5.0	0.90	0.2

END PWAT-PARM4

PWAT-STATE1

*** < PLS>	PWATER state variables (in)						
*** x - x	CEPS	SURS	UZS	IFWS	LZS	AGWS	
GWVS							
101 607	0.0	0.00	0.9	0.00	9.4		1

0.00

END PWAT-STATE1

MON-INTERCEP

*** <PLS >	Interception storage capacity at start of each month (in)												
*** x - x	JAN	FEB	MAR	APR	MAY	JUN	JUL	AUG	SEP	OCT	NOV	DEC	
101 109	0.20	0.20	0.20	0.20	0.20	0.20	0.20	0.20	0.20	0.20	0.20	0.20	0.20
201 206	0.20	0.20	0.20	0.20	0.20	0.22	0.22	0.22	0.20	0.20	0.20	0.20	0.20
301 309	0.15	0.15	0.15	0.15	0.15	0.16	0.16	0.16	0.16	0.16	0.16	0.16	0.16
401 409	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05
607	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01

END MON-INTERCEP

MON-UZSN

```
*** <PLS > Upper zone storage at start of each month (inches)
*** x - x JAN FEB MAR APR MAY JUN JUL AUG SEP OCT NOV DEC
101 109 1.10 1.10 1.10 1.00 1.00 1.00 1.00 1.00 1.00 1.10 1.10 1.10
201 206 1.10 1.10 1.10 1.00 1.00 1.00 1.00 1.00 1.00 1.10 1.10 1.10
301 309 1.10 1.10 1.10 1.00 1.00 1.00 1.00 1.00 1.00 1.10 1.10 1.10
401 409 1.10 1.10 1.10 1.00 1.00 1.00 1.00 1.00 1.00 1.10 1.10 1.10
607 1.10 1.10 1.10 1.00 1.00 1.00 1.00 1.00 1.00 1.10 1.10 1.10
END MON-UZSN
```

MON-LZETPARM

```
*** <PLS > Lower zone evapotransp parm at start of each month
*** x - x JAN FEB MAR APR MAY JUN JUL AUG SEP OCT NOV DEC
101 109 0.65 0.65 0.65 0.65 0.65 0.66 0.66 0.66 0.65 0.65 0.65 0.65
201 206 0.40 0.40 0.40 0.40 0.40 0.40 0.40 0.40 0.40 0.40 0.40 0.40
301 309 0.40 0.40 0.40 0.40 0.40 0.40 0.40 0.40 0.40 0.40 0.40 0.40
401 409 0.20 0.20 0.20 0.20 0.20 0.20 0.20 0.20 0.20 0.20 0.20 0.20
607 0.20 0.20 0.20 0.20 0.20 0.20 0.20 0.20 0.20 0.20 0.20 0.20
END MON-LZETPARM
```

*** Section SEDMNT ***

SED-PARM1

```
<PLS >***
# - # CRV VSIV SDOP ***
101 607 1 0 1
END SED-PARM1
```

SED-PARM2

```
*** <PLS > SMPF KRER JRER AFFIX COVER NVSI
*** x - x (/day) lb/ac-day
101 109 1.000 0.268 2.000 0.010 0.000 1.000
201 206 1.000 0.300 2.000 0.010 0.000 1.000
301 309 1.000 0.310 2.000 0.010 0.000 1.000
401 409 1.000 0.300 2.000 0.010 0.000 1.000
607 1.000 0.100 2.000 0.010 0.000 1.000
END SED-PARM2
```

SED-PARM3

```
*** <PLS > Sediment parameter 3
*** x - x KSER JSER KGER JGER
101 109 5.0000 1.10 0.000 2.00
201 206 10.000 0.90 10.00 1.00
301 309 8.5000 1.10 1.000 1.00
401 409 10.000 1.60 0.000 2.00
607 05.000 1.60 0.000 2.00
END SED-PARM3
```

MON-COVER

```
# - # JAN FEB MAR APR MAY JUN JUL AUG SEP OCT NOV DEC
***
101 109 .920 .920 .920 .920 .970 .970 .970 .970 .970 .920 .920 .920
201 206 .350 .340 .230 .270 .370 .440 .740 .920 .920 .520 .430 .370
301 309 .875 .875 .875 .910 .930 .930 .890 .890 .890 .880 .875 .875
401 409 .900 .900 .900 .910 .930 .930 .930 .930 .930 .910 .900 .900
```

607 .900 .900 .900 .910 .930 .930 .930 .930 .930 .910 .900 .900
 END MON-COVER

SED-STOR

#	#	DETS
101	109	0.03
201	206	0.70
301	309	0.01
401	409	0.03
607		0.03

END SED-STOR

*** section GQUAL (for fecal indicator bacteria)

NQUALS

#	#NQUAL	***
101	607	1

END NQUALS

QUAL-PROPS

*** <PLS > Identifiers and Flags

***	x	-	x	QUALID	QTID	QSD	VPFW	VPFS	QSO	VQO	QIFW	VIQC	QAGW
VAQC	101		607FC		#	1	2	0	1	1	1	0	1
	0												

END QUAL-PROPS

QUAL-INPUT

*** Storage on surface and nonseasonal parameters

***		SQO	POTFW	POTFS	ACQOP	SQOLIM	WSQOP	IOQC	AOQC
*** <PLS >		qty/ac	qty/ton	qty/ton	qty/	qty/ac	in/hr	qty/ft3	qty/ft3
*** x - x					ac.day				
101	109	0E+10	0.	0.	1E+10	9E+10	2.00	177.	118.
201	203	0E+10	0.	0.	1E+10	9E+10	0.20	531.	354.
204	206	0E+10	0.	0.	1E+10	9E+10	0.10	531.	354.
301	303	0E+10	0.	0.	1E+10	9E+10	0.20	177.	118.
304	309	0E+10	0.	0.	1E+10	9E+10	0.10	177.	118.
401	403	0E+10	0.	0.	1E+10	9E+10	0.10	531.	354.
404	409	0E+10	0.	0.	1E+10	9E+10	0.01	531.	354.
607		0E+10	0.	0.	1E+10	9E+10	0.10	531.	354.

END QUAL-INPUT

MON-POTFW

#	#	JAN	FEB	MAR	APR	MAY	JUN	JUL	AUG	SEP	OCT	NOV	DEC
101	109	.030	.010	.180	.060	.120	.302	.201	.804	.400	.120	.240	.015
201	209	2.55	0.43	0.50	1.59	3.17	4.75	3.17	2.66	3.17	3.17	2.66	1.28
301	309	2.55	0.43	0.50	1.59	3.17	4.75	3.17	2.66	3.17	3.17	2.66	1.28
401	409	.21	.28	.48	1.28	2.57	1.93	2.57	5.14	0.28	1.24	1.24	.42
607													

END MON-POTFW

MON-ACCUM

*** <PLS > Value at start of each month for accum rate of QUALOF
 (#/ac.day)

```

*** x - x JAN FEB MAR APR MAY JUN JUL AUG SEP OCT NOV DEC
*** N22-1
201 12E0612E0611E0712E0711E0712E0612E0612E0612E0630E0631E0612E06
301 15E0716E0717E0717E0717E0717E0718E0718E0718E0714E0714E0714E07
401 53E0753E0753E0753E0753E0753E0753E0753E0753E0753E0753E07
101 12E0612E0612E0612E0612E0612E0612E0612E0612E0612E0612E06
*** N22-2
202 60E0560E0589E0592E0591E0560E0560E0560E0560E0566E0565E0560E05
302 60E0560E0580E0582E0581E0560E0560E0560E0582E0581E0580E0560E05
402 68E0768E0768E0768E0768E0768E0768E0768E0768E0768E0768E07
102 66E0566E0566E0566E0566E0566E0566E0566E0566E0566E0566E0566E05
*** N22-3
203 16E0616E0616E0816E0816E0816E0616E0616E0616E0630E0730E0716E06
303 14E0916E0916E0916E0917E0917E0917E0918E0918E0913E0913E0913E09
403 26E0726E0726E0726E0726E0726E0726E0726E0726E0726E0726E0726E07
103 16E0616E0616E0616E0616E0616E0616E0616E0616E0616E0616E0616E06
*** N22-4
204 29E0629E0628E0729E0728E0729E0629E0629E0629E0675E0677E0629E06
304 38E0842E0843E0844E0845E0845E0846E0847E0848E0835E0836E0837E08
404 47E0747E0747E0747E0747E0747E0747E0747E0747E0747E0747E0747E07
104 33E0633E0633E0633E0633E0633E0633E0633E0633E0633E0633E0633E06
*** N22-5
205 20E0620E0611E0811E0811E0820E0620E0620E0620E0622E0722E0720E06
305 83E0894E0897E0810E0910E0910E0911E0911E0911E0977E0880E0881E08
405 11E0811E0811E0811E0811E0811E0811E0811E0811E0811E0811E0811E08
105 22E0622E0622E0622E0622E0622E0622E0622E0622E0622E0622E0622E06
*** N22-6
206 45E0645E0685E0787E0785E0745E0645E0645E0645E0619E0720E0745E06
306 11E1012E1013E1013E1013E1013E1014E1014E1014E1099E0910E1011E10
406 13E0713E0713E0713E0713E0713E0713E0713E0713E0713E0713E0713E07
106 45E0645E0645E0645E0645E0645E0645E0645E0645E0645E0645E0645E06
*** N22-7
407 59E0759E0759E0759E0759E0759E0759E0759E0759E0759E0759E0759E07
*** N22-8
308 42E0642E0644E0644E0644E0642E0642E0642E0644E0644E0644E0642E06
408 18E0818E0818E0818E0818E0818E0818E0818E0818E0818E0818E0818E08
108 46E0646E0646E0646E0646E0646E0646E0646E0646E0646E0646E0646E06
*** N22-9
309 66E0666E0668E0668E0668E0666E0666E0666E0668E0668E0668E0666E06
409 33E0833E0833E0833E0833E0833E0833E0833E0833E0833E0833E0833E08
109 13E0713E0713E0713E0713E0713E0713E0713E0713E0713E0713E0713E07
END MON-ACCUM

```

MON-SQOLIM

```

*** <PLS > Value at start of month for limiting storage of QUALOF (#/ac)
*** x - x JAN FEB MAR APR MAY JUN JUL AUG SEP OCT NOV DEC
*** N22-1
201 11E0711E0710E0811E0810E0811E0711E0711E0711E0727E0728E0711E07
301 13E0815E0815E0815E0816E0816E0816E0816E0817E0813E0813E0813E08
401 48E0848E0848E0848E0848E0848E0848E0848E0848E0848E0848E0848E08
101 11E0711E0711E0711E0711E0711E0711E0711E0711E0711E0711E0711E07
*** N22-2
202 54E0654E0681E0683E0682E0654E0654E0654E0654E0659E0659E0654E06
302 54E0654E0672E0673E0673E0654E0654E0654E0673E0673E0672E0654E06

```

```

402      61E0861E0861E0861E0861E0861E0861E0861E0861E0861E0861E08
102      59E0659E0659E0659E0659E0659E0659E0659E0659E0659E0659E06
*** N22-3
203      14E0714E0714E0914E0914E0914E0714E0714E0714E0727E0827E0814E07
303      12E1014E1014E1015E1015E1015E1016E1016E1016E1011E1012E1012E10
403      24E0824E0824E0824E0824E0824E0824E0824E0824E0824E0824E0824E08
103      15E0715E0715E0715E0715E0715E0715E0715E0715E0715E0715E0715E07
*** N22-4
204      26E0726E0725E0826E0825E0826E0726E0726E0726E0726E0768E0769E0726E07
304      34E0938E0939E0939E0940E0941E0941E0942E0943E0932E0933E0933E09
404      42E0842E0842E0842E0842E0842E0842E0842E0842E0842E0842E0842E08
104      30E0730E0730E0730E0730E0730E0730E0730E0730E0730E0730E0730E0730E07
*** N22-5
205      18E0718E0710E0910E0910E0918E0718E0718E0718E0720E0820E0818E07
305      75E0984E0988E0990E0991E0993E0995E0997E0999E0970E0972E0973E09
405      10E0910E0910E0910E0910E0910E0910E0910E0910E0910E0910E0910E09
105      20E0720E0720E0720E0720E0720E0720E0720E0720E0720E0720E0720E0720E07
*** N22-6
206      41E0741E0776E0879E0876E0841E0741E0741E0741E0717E0818E0841E07
306      99E1011E1111E1112E1112E1112E1112E1112E1113E1113E1189E1093E1096E10
406      12E0812E0812E0812E0812E0812E0812E0812E0812E0812E0812E0812E0812E08
106      41E0741E0741E0741E0741E0741E0741E0741E0741E0741E0741E0741E0741E07
*** N22-7
407      53E0853E0853E0853E0853E0853E0853E0853E0853E0853E0853E0853E08
*** N22-8
308      38E0738E0740E0740E0740E0738E0738E0738E0740E0740E0740E0738E07
408      16E0916E0916E0916E0916E0916E0916E0916E0916E0916E0916E0916E09
108      41E0741E0741E0741E0741E0741E0741E0741E0741E0741E0741E0741E0741E07
*** N22-9
309      59E0759E0761E0761E0761E0759E0759E0759E0761E0761E0761E0759E07
409      29E0929E0929E0929E0929E0929E0929E0929E0929E0929E0929E0929E09
109      11E0811E0811E0811E0811E0811E0811E0811E0811E0811E0811E0811E08

```

END MON-SQOLIM

END PERLND

IMPLND

ACTIVITY

```

*** <ILS >           Active Sections
*** x - x ATMP SNOW IWAT  SLD  IWG IQAL
101      0      0      1      1      0      1
END ACTIVITY

```

PRINT-INFO

```

*** <ILS > ***** Print-flags ***** PIVL  PYR
*** x - x ATMP SNOW IWAT  SLD  IWG IQAL *****
101      4      4      4      4      4      4      1      9
END PRINT-INFO

```

GEN-INFO

```

***      Name           Unit-systems   Printer BinaryOut
*** <ILS >           t-series   Engl Metr Engl Metr
*** x - x           in   out
101      1      1      0      0      0      0
END GEN-INFO

```

```

IWAT-PARM1
*** <ILS >          Flags
*** x - x CSNO RTOP  VRS  VNN RTLI
    101          0    1    0    0    0
END IWAT-PARM1

IWAT-PARM2
*** <ILS >          LSUR          SLSUR          NSUR          RETSC
*** x - x          (ft)          (in)
    101  106      100.          0.150          0.10          0.150
    107          100.          0.150          0.10          0.300
    108  109      100.          0.150          0.10          0.250
END IWAT-PARM2

IWAT-PARM3
*** <ILS >          PETMAX          PETMIN
*** x - x          (deg F)          (deg F)
    101          40.          35.
END IWAT-PARM3

IWAT-STATE1
*** <ILS >  IWATER state variables (inches)
*** x - x          RETS          SURS
    101          0.0          0.00
END IWAT-STATE1

SLD-PARM1
  <PLS >***
  # - # VASD VRSD SDOP ***
    101          0    0    1
END SLD-PARM1

SLD-PARM2
***          KEIM          JEIM          ACCSDP          REMSDP
*** <ILS >          tons/          /day
*** x - x          ac.day
***
    101          0.10          2.0          0.0005          0.60
END SLD-PARM2

SLD-STOR
*** <ILS >  Solids storage (tons/acre)
*** x - x
    101          0.1
END SLD-STOR

*** FIB section for IMPLND
NQUALS
  #          #NQUAL ***
    101          1
END NQUALS

QUAL-PROPS

```

```

*** <ILS >
*** x - x      QUALID      QTID      QSD VPFW      QSO      VQO
    101      FC              #          0      0      1      0
END QUAL-PROPS

QUAL-INPUT
***          Storage on surface and nonseasonal parameters
***          SQO      POTFW      ACQOP      SQOLIM      WSQOP
*** <ILS >  qty/ac qty/ton      qty/      qty/ac      in/hr
*** x - x              ac.day
    101          1E+07      0.      1E+07      3E+07      0.01
END QUAL-INPUT
END IMPLND

RCHRES
ACTIVITY
*** RCHRES  Active sections
*** x - x  HYFG ADFG CNFG HTFG SDFG GQFG OXFG NUFG PKFG PHFG
    1      9      1      1      0      0      1      1      0      0      0      0
END ACTIVITY

PRINT-INFO
*** RCHRES  Printout level flags
*** x - x  HYDR ADCA CONS HEAT SED      GQL OXRX NUTR PLNK PHCB PIVL PYR
    1      9      4      4      4      4      4      4      4      4      4      1      9
END PRINT-INFO

GEN-INFO
***          Name          Nexits      Unit Systems      Printer
*** RCHRES          t-series  Engl Metr LKFG
*** x - x          in out
    1      9      StroublesCrk          1          1      1      0      0      0      0
0
END GEN-INFO

HYDR-PARM1
***          Flags for HYDR section
***RC HRES  VC A1 A2 A3      ODFVFG for each *** ODGTFG for each      FUNCT
for each
*** x - x  FG FG FG FG      possible      exit *** possible      exit      possible
exit
    1      9      0      1      1      1      4      0      0      0      0          0      0      0      0      0      1      1      1
1 1
END HYDR-PARM1

HYDR-PARM2
*** RCHRES  FTBW FTBU          LEN          DELTH          STCOR          KS          DB50
*** x - x          (miles)      (ft)          (ft)          KS          (in)
    1          0.      1          2.29          119.7          3.2          0.5          0.01
    2          0.      2          2.41          62.91          3.2          0.5          0.01
    3          0.      3          0.49          6.7          3.2          0.5          0.01
    4          0.      4          0.54          7.17          3.2          0.5          0.01
    5          0.      5          0.80          16.28          3.2          0.5          0.01
    6          0.      6          0.62          17.07          3.2          0.5          0.01

```

7	0.	7	0.28	7.87	3.2	0.5	0.01
8	0.	8	1.30	90.65	3.2	0.5	0.01
9	0.	9	1.78	173.9	3.2	0.5	0.01

END HYDR-PARM2

MON-CONVF

*** RCHRES Monthly f(VOL) adjustment factors

*** x - x	JAN	FEB	MAR	APR	MAY	JUN	JUL	AUG	SEP	OCT	NOV	DEC
1 9	0.90	0.89	0.89	0.91	0.93	1.99	1.99	1.99	0.99	0.98	0.98	0.90

END MON-CONVF

HYDR-INIT

*** Initial conditions for HYDR section

*** RCHRES VOL CAT Initial value of COLIND initial value of OUTDGT

*** x - x	ac-ft	for each possible exit					for each possible exit,ft3		
1 9	10.0	4.2	4.5	4.5	4.5	4.2	2.1	1.2	0.5
		1.2	1.8						

END HYDR-INIT

SANDFG

*** RCHRES

*** x - x	SNDFG
1 9	3

END SANDFG

SED-GENPARM

*** x - x (ft) (ft)

*** BEDWID is the effective width over which bed sediment is deposited; BEDWRN is the depth of sediment in the bed

*** The channel width at low flow: 2.7-4.0 m (8.8-13.1 ft)

*** The water depth at low flow: 0.1-0.3 m (0.3-1 ft)

*** Porosity estimation: 0.3-0.7

RCHRES	BEDWID	BEDWRN	POR	***
# - #				***
1 6	09.0	0.3	0.4	
7	09.0	3.0	0.4	
8 9	09.0	0.3	0.4	

END SED-GENPARM

SAND-PM

*** RCHRES	D	W	RHO	KSAND	EXPSND
*** x - x	(in)	(in/sec)	(g/cm3)		
1 9	0.01	0.25	2.6	0.1	2.0

END SAND-PM

SILT-CLAY-PM

RCHRES	D	W	RHO	TAUCD	TAUCS	M	***
# - #							***
1	0.0003	0.0005	2.30	0.034	0.123	0.01	
2	0.0003	0.0005	2.30	0.021	0.114	0.01	
3	0.0003	0.0005	2.30	0.014	0.078	0.01	
4	0.0003	0.0005	2.30	0.012	0.044	0.01	

5	0.0003	0.0005	2.30	0.014	0.056	0.01
6	0.0003	0.0005	2.30	0.024	0.127	0.01
7	0.0003	0.0005	2.30	0.582	0.620	0.01
8	0.0003	0.0005	2.30	0.032	0.10	0.01
9	0.0003	0.0005	2.30	0.039	0.184	0.01

END SILT-CLAY-PM

SILT-CLAY-PM

RCHRES	D	W	RHO	TAUCD	TAUCS	M ***
# - #						***
1	0.0001	0.00005	2.00	0.028	0.11	0.01
2	0.0001	0.00005	2.00	0.018	0.072	0.01
3	0.0001	0.00005	2.00	0.012	0.047	0.01
4	0.0001	0.00005	2.00	0.01	0.035	0.01
5	0.0001	0.00005	2.00	0.012	0.047	0.01
6	0.0001	0.00005	2.00	0.021	0.07	0.01
7	0.0001	0.00005	2.00	0.580	0.610	0.01
8	0.0001	0.00005	2.00	0.029	0.072	0.01
9	0.0001	0.00005	2.00	0.037	0.108	0.01

END SILT-CLAY-PM

SSSED-INIT

RCHRES	Suspended sed concs (mg/l) ***		
# - #	Sand	Silt	Clay ***
1 9	0.	8.	8.

END SSSED-INIT

BED-INIT

*** Initial conditions
 *** The soil from the full vertical profile of a stream bank: 23% sand, 54% silt, 23% clay. (Tyler's Thesis, pg54).
 *** Based on the Tech Note 8 (page33), the fractions should reflect the relative percent of sand, silt, clay available for erosion in the watershed,
 *** but should also include an enrichment factor of silt and clay to represent the likelihood of these finer materials reaching the channel.
 ***Thus, the sand would be somewhat transport limited, compared to the silt and clay.

RCHRES	BEDDEP	Initial bed composition			***
# - #	(ft)	Sand	Silt	Clay	***
1 6	0.2	.05	.60	.35	
7	1	.05	.60	.35	
8 9	0.2	.05	.60	.35	

END BED-INIT

FIB section*****

GQ-QALDATA

RCHRES	GQID	DQAL	CONCID	CONV	QTYID
x - x		concid			
1 9FC		100.	#/10	0.0035	#

END GQ-QALDATA

GQ-QALFG

```

*** x - x
    1   9   0   0   0   0   0   1   1
END GQ-QALFG

GQ-GENDECAY
*** RCHRES      FSTDEC      THFST
*** x - x      (/day)
    1   3      1.15      1.05
    7           4.00      1.05
    4   9      1.15      1.05
END GQ-GENDECAY

***Bacteria-sediment association
GQ-SEDCONC
***<range><-----sedconc----->
*** RCHRES      1-3: suspend sand silt clay; 4-6 bed sand silt clay
*** x - x      SQAL1      SQAL2      SQAL3      SQAL4      SQAL5      SQAL6
    1   9      0.01      10.      10.      0.001      0.1      0.1
END GQ-SEDCONC

GQ-KD
***<range><-----k-part----->
*** RCHRES      1-3: suspend sand silt clay; 4-6 bed sand silt clay
*** x - x      ADPM1      ADPM2      ADPM3      ADPM4      ADPM5      ADPM6
    1   9      1.0E-8      0.5      0.5      1.0E-8      0.0005      0.0005
END GQ-KD

GQ-ADRATE
***<range><-----k-adsdes----->
*** RCHRES      1-3: suspend sand silt clay; 4-6 bed sand silt clay
*** x - x      ADPM1      ADPM2      ADPM3      ADPM4      ADPM5      ADPM6
    1   9      1.0E-4      10000      10000      1.0E-4      1000      1000
END GQ-ADRATE

GQ-SEDDCAY
***<range><-----ads-decay----->
*** RCHRES      KSUSP      THSUSP      KBED      THBED
*** x - x      (/day)      (/day)
    1   9      0.6      1.06      0.20      1.03
END GQ-SEDDCAY

END RCHRES

FTABLES
FTABLE      1
rows cols
    4      4
    depth      area      volume      outflow1 ***
        0.      5.22      0.      0.
        0.01      5.22      0.05      0.
        2.93      11.55      24.61      476.35
        45.59      601.48      1773.82      169167.
END FTABLE      1

```

```

FTABLE      2
rows cols          ***
  4      4
    depth      area      volume      outflow1 ***
      0.      19.43      0.      0.
     0.01      19.43      0.19      0.
      1.9      19.2      36.68      252.84
     83.92     437.52     25063.55 1006730.09
END FTABLE  2

```

```

FTABLE      3
rows cols          ***
  4      4
    depth      area      volume      outflow1 ***
      0.      3.38      0.      0.
     0.01      3.38      0.03      0.
      1.76      3.34      5.9      203.87
      28.      47.32     853.68     64940.09
END FTABLE  3

```

```

FTABLE      4
rows cols          ***
  4      4
    depth      area      volume      outflow1 ***
      0.      3.59      0.      0.
     0.01      3.59      0.04      0.
      1.66      3.54      5.92      174.8
     25.28     71.51     901.73     44353.9
END FTABLE  4

```

```

FTABLE      5
rows cols          ***
  4      4
    depth      area      volume      outflow1 ***
      0.      5.12      0.      0.
     0.01      5.12      0.05      0.
      1.63      5.05      8.3      166.84
     11.48     95.09     569.86     13866.32
END FTABLE  5

```

```

FTABLE      6
rows cols          ***
  4      4
    depth      area      volume      outflow1 ***
      0.      3.38      0.      0.
     0.01      3.38      0.03      0.
      1.44      3.32      4.83      118.21
     11.61     143.71     940.84     22476.73
END FTABLE  6

```

```

FTABLE      7
rows cols          ***
  7      4
    depth      area      volume      outflow1 ***

```

0.	0.00	0.	0.
1.46	1.82	2.2568	0.405
2.92	3.82	6.2568	0.567
6.84	4.64	8.9544	2.066
9.84	7.28	9.5630	2000
14.84	7.30	34.383	6000
31.01	338.78	3848.03	30707.05

END FTABLE 7

FTABLE 8

rows	cols	***		
4	4			
depth	area	volume	outflow1	***
0.	2.51	0.	0.	
0.01	2.51	0.03	0.	
1.16	2.46	2.89	65.36	
25.77	186.12	2992.61	295449.88	

END FTABLE 8

FTABLE 9

rows	cols	***		
4	4			
depth	area	volume	outflow1	***
0.	5.43	0.	0.	
0.01	5.43	0.05	0.	
1.01	5.31	5.43	44.58	
11.84	132.28	848.34	19856.96	

END FTABLE 9

END FTABLES

NETWORK

*** Cattle

MUTSIN	01	OUTPUT	01	1.0	SAME	RCHRES	01	INFLOW	IDQAL
MUTSIN	01	OUTPUT	02	1.0	SAME	RCHRES	02	INFLOW	IDQAL
MUTSIN	01	OUTPUT	03	1.0	SAME	RCHRES	03	INFLOW	IDQAL
MUTSIN	01	OUTPUT	04	1.0	SAME	RCHRES	04	INFLOW	IDQAL
MUTSIN	01	OUTPUT	05	1.0	SAME	RCHRES	05	INFLOW	IDQAL
MUTSIN	01	OUTPUT	06	1.0	SAME	RCHRES	06	INFLOW	IDQAL
MUTSIN	01	OUTPUT	07	1.0	SAME	RCHRES	07	INFLOW	IDQAL
MUTSIN	01	OUTPUT	08	1.0	SAME	RCHRES	08	INFLOW	IDQAL
MUTSIN	01	OUTPUT	09	1.0	SAME	RCHRES	09	INFLOW	IDQAL

*** Wildlife

MUTSIN	02	OUTPUT	01	1.0	SAME	RCHRES	01	INFLOW	IDQAL
MUTSIN	02	OUTPUT	02	1.0	SAME	RCHRES	02	INFLOW	IDQAL
MUTSIN	02	OUTPUT	03	1.0	SAME	RCHRES	03	INFLOW	IDQAL
MUTSIN	02	OUTPUT	04	1.0	SAME	RCHRES	04	INFLOW	IDQAL
MUTSIN	02	OUTPUT	05	1.0	SAME	RCHRES	05	INFLOW	IDQAL
MUTSIN	02	OUTPUT	06	1.0	SAME	RCHRES	06	INFLOW	IDQAL
MUTSIN	02	OUTPUT	07	1.0	SAME	RCHRES	07	INFLOW	IDQAL
MUTSIN	02	OUTPUT	08	1.0	SAME	RCHRES	08	INFLOW	IDQAL
MUTSIN	02	OUTPUT	09	1.0	SAME	RCHRES	09	INFLOW	IDQAL

*** Straight Pipes

MUTSIN	03	OUTPUT	01	1.0	SAME	RCHRES	01	INFLOW	IDQAL
MUTSIN	03	OUTPUT	02	1.0	SAME	RCHRES	02	INFLOW	IDQAL

MUTSIN	03	OUTPUT	03	1.0	SAME	RCHRES	03	INFLOW	IDQAL
MUTSIN	03	OUTPUT	04	1.0	SAME	RCHRES	04	INFLOW	IDQAL
MUTSIN	03	OUTPUT	05	1.0	SAME	RCHRES	05	INFLOW	IDQAL
MUTSIN	03	OUTPUT	06	1.0	SAME	RCHRES	06	INFLOW	IDQAL
MUTSIN	03	OUTPUT	07	1.0	SAME	RCHRES	07	INFLOW	IDQAL
MUTSIN	03	OUTPUT	08	1.0	SAME	RCHRES	08	INFLOW	IDQAL
MUTSIN	03	OUTPUT	09	1.0	SAME	RCHRES	09	INFLOW	IDQAL
*** PReP Spills into Reaches				1.0					
MUTSIN	20	OUTPUT	01	1.0	SAME	RCHRES	05	INFLOW	IVOL
MUTSIN	20	OUTPUT	02	1.0	SAME	RCHRES	05	INFLOW	IDQAL
MUTSIN	20	OUTPUT	03	1.0	SAME	RCHRES	07	INFLOW	IVOL
MUTSIN	20	OUTPUT	04	1.0	SAME	RCHRES	07	INFLOW	IDQAL
MUTSIN	20	OUTPUT	05	1.0	SAME	RCHRES	08	INFLOW	IVOL
MUTSIN	20	OUTPUT	06	1.0	SAME	RCHRES	08	INFLOW	IDQAL
MUTSIN	20	OUTPUT	07	1.0	SAME	RCHRES	09	INFLOW	IVOL
MUTSIN	20	OUTPUT	08	1.0	SAME	RCHRES	09	INFLOW	IDQAL
RCHRES	9	SEDTRN	RSED	5		PLTGEN	1	INPUT	MEAN 1
RCHRES	8	SEDTRN	RSED	5		PLTGEN	1	INPUT	MEAN 2
RCHRES	7	SEDTRN	RSED	5		PLTGEN	1	INPUT	MEAN 3
RCHRES	6	SEDTRN	RSED	5		PLTGEN	1	INPUT	MEAN 4
RCHRES	5	SEDTRN	RSED	5		PLTGEN	1	INPUT	MEAN 5
RCHRES	4	SEDTRN	RSED	5		PLTGEN	1	INPUT	MEAN 6
RCHRES	3	SEDTRN	RSED	5		PLTGEN	1	INPUT	MEAN 7
RCHRES	2	SEDTRN	RSED	5		PLTGEN	1	INPUT	MEAN 8
RCHRES	1	SEDTRN	RSED	5		PLTGEN	1	INPUT	MEAN 9
RCHRES	9	SEDTRN	ISED	4		PLTGEN	7	INPUT	MEAN 1
RCHRES	8	SEDTRN	ISED	4		PLTGEN	7	INPUT	MEAN 2
RCHRES	7	SEDTRN	ISED	4		PLTGEN	7	INPUT	MEAN 3
RCHRES	6	SEDTRN	ISED	4		PLTGEN	7	INPUT	MEAN 4
RCHRES	5	SEDTRN	ISED	4		PLTGEN	7	INPUT	MEAN 5
RCHRES	4	SEDTRN	ISED	4		PLTGEN	7	INPUT	MEAN 6
RCHRES	3	SEDTRN	ISED	4		PLTGEN	7	INPUT	MEAN 7
RCHRES	2	SEDTRN	ISED	4		PLTGEN	7	INPUT	MEAN 8
RCHRES	1	SEDTRN	ISED	4		PLTGEN	7	INPUT	MEAN 9
RCHRES	9	SEDTRN	ROSED	4		PLTGEN	5	INPUT	MEAN 1
RCHRES	8	SEDTRN	ROSED	4		PLTGEN	5	INPUT	MEAN 2
RCHRES	7	SEDTRN	ROSED	4		PLTGEN	5	INPUT	MEAN 3
RCHRES	6	SEDTRN	ROSED	4		PLTGEN	5	INPUT	MEAN 4
RCHRES	5	SEDTRN	ROSED	4		PLTGEN	5	INPUT	MEAN 5
RCHRES	4	SEDTRN	ROSED	4		PLTGEN	5	INPUT	MEAN 6
RCHRES	3	SEDTRN	ROSED	4		PLTGEN	5	INPUT	MEAN 7
RCHRES	2	SEDTRN	ROSED	4		PLTGEN	5	INPUT	MEAN 8
RCHRES	1	SEDTRN	ROSED	4		PLTGEN	5	INPUT	MEAN 9
RCHRES	9	SEDTRN	DEPSCR	3		PLTGEN	6	INPUT	MEAN 1
RCHRES	8	SEDTRN	DEPSCR	3		PLTGEN	6	INPUT	MEAN 2
RCHRES	7	SEDTRN	DEPSCR	3		PLTGEN	6	INPUT	MEAN 3
RCHRES	6	SEDTRN	DEPSCR	3		PLTGEN	6	INPUT	MEAN 4
RCHRES	5	SEDTRN	DEPSCR	3		PLTGEN	6	INPUT	MEAN 5
RCHRES	4	SEDTRN	DEPSCR	3		PLTGEN	6	INPUT	MEAN 6
RCHRES	3	SEDTRN	DEPSCR	3		PLTGEN	6	INPUT	MEAN 7
RCHRES	2	SEDTRN	DEPSCR	3		PLTGEN	6	INPUT	MEAN 8
RCHRES	1	SEDTRN	DEPSCR	3		PLTGEN	6	INPUT	MEAN 9
RCHRES	9	HYDR	TAU			PLTGEN	3	INPUT	MEAN 1
RCHRES	8	HYDR	TAU			PLTGEN	3	INPUT	MEAN 2

RCHRES	7	HYDR	TAU			PLTGEN	3	INPUT	MEAN	3
RCHRES	6	HYDR	TAU			PLTGEN	3	INPUT	MEAN	4
RCHRES	5	HYDR	TAU			PLTGEN	3	INPUT	MEAN	5
RCHRES	4	HYDR	TAU			PLTGEN	3	INPUT	MEAN	6
RCHRES	3	HYDR	TAU			PLTGEN	3	INPUT	MEAN	7
RCHRES	2	HYDR	TAU			PLTGEN	3	INPUT	MEAN	8
RCHRES	1	HYDR	TAU			PLTGEN	3	INPUT	MEAN	9
RCHRES	9	SEDTRN	SSED	3		PLTGEN	4	INPUT	MEAN	1
RCHRES	8	SEDTRN	SSED	3		PLTGEN	4	INPUT	MEAN	2
RCHRES	7	SEDTRN	SSED	3		PLTGEN	4	INPUT	MEAN	3
RCHRES	6	SEDTRN	SSED	3		PLTGEN	4	INPUT	MEAN	4
RCHRES	5	SEDTRN	SSED	3		PLTGEN	4	INPUT	MEAN	5
RCHRES	4	SEDTRN	SSED	3		PLTGEN	4	INPUT	MEAN	6
RCHRES	3	SEDTRN	SSED	3		PLTGEN	4	INPUT	MEAN	7
RCHRES	2	SEDTRN	SSED	3		PLTGEN	4	INPUT	MEAN	8
RCHRES	1	SEDTRN	SSED	3		PLTGEN	4	INPUT	MEAN	9
RCHRES	9	SEDTRN	BEDDEP			PLTGEN	2	INPUT	MEAN	1
RCHRES	8	SEDTRN	BEDDEP			PLTGEN	2	INPUT	MEAN	2
RCHRES	7	SEDTRN	BEDDEP			PLTGEN	2	INPUT	MEAN	3
RCHRES	6	SEDTRN	BEDDEP			PLTGEN	2	INPUT	MEAN	4
RCHRES	5	SEDTRN	BEDDEP			PLTGEN	2	INPUT	MEAN	5
RCHRES	4	SEDTRN	BEDDEP			PLTGEN	2	INPUT	MEAN	6
RCHRES	3	SEDTRN	BEDDEP			PLTGEN	2	INPUT	MEAN	7
RCHRES	2	SEDTRN	BEDDEP			PLTGEN	2	INPUT	MEAN	8
RCHRES	1	SEDTRN	BEDDEP			PLTGEN	2	INPUT	MEAN	9
RCHRES	9	HYDR	RO			PLTGEN	8	INPUT	MEAN	1
RCHRES	8	HYDR	RO			PLTGEN	8	INPUT	MEAN	2
RCHRES	7	HYDR	RO			PLTGEN	8	INPUT	MEAN	3
RCHRES	6	HYDR	RO			PLTGEN	8	INPUT	MEAN	4
RCHRES	5	HYDR	RO			PLTGEN	8	INPUT	MEAN	5
RCHRES	4	HYDR	RO			PLTGEN	8	INPUT	MEAN	6
RCHRES	3	HYDR	RO			PLTGEN	8	INPUT	MEAN	7
RCHRES	2	HYDR	RO			PLTGEN	8	INPUT	MEAN	8
RCHRES	1	HYDR	RO			PLTGEN	8	INPUT	MEAN	9
RCHRES	9	GQUAL	SQAL	2		PLTGEN	9	INPUT	MEAN	1
RCHRES	8	GQUAL	SQAL	2		PLTGEN	9	INPUT	MEAN	2
RCHRES	7	GQUAL	SQAL	2		PLTGEN	9	INPUT	MEAN	3
RCHRES	6	GQUAL	SQAL	2		PLTGEN	9	INPUT	MEAN	4
RCHRES	5	GQUAL	SQAL	2		PLTGEN	9	INPUT	MEAN	5
RCHRES	4	GQUAL	SQAL	2		PLTGEN	9	INPUT	MEAN	6
RCHRES	3	GQUAL	SQAL	2		PLTGEN	9	INPUT	MEAN	7
RCHRES	2	GQUAL	SQAL	2		PLTGEN	9	INPUT	MEAN	8
RCHRES	1	GQUAL	SQAL	2		PLTGEN	9	INPUT	MEAN	9
RCHRES	9	GQUAL	SQAL	3		PLTGEN	10	INPUT	MEAN	1
RCHRES	8	GQUAL	SQAL	3		PLTGEN	10	INPUT	MEAN	2
RCHRES	7	GQUAL	SQAL	3		PLTGEN	10	INPUT	MEAN	3
RCHRES	6	GQUAL	SQAL	3		PLTGEN	10	INPUT	MEAN	4
RCHRES	5	GQUAL	SQAL	3		PLTGEN	10	INPUT	MEAN	5
RCHRES	4	GQUAL	SQAL	3		PLTGEN	10	INPUT	MEAN	6
RCHRES	3	GQUAL	SQAL	3		PLTGEN	10	INPUT	MEAN	7
RCHRES	2	GQUAL	SQAL	3		PLTGEN	10	INPUT	MEAN	8
RCHRES	1	GQUAL	SQAL	3		PLTGEN	10	INPUT	MEAN	9
RCHRES	9	GQUAL	SQAL	5		PLTGEN	11	INPUT	MEAN	1
RCHRES	8	GQUAL	SQAL	5		PLTGEN	11	INPUT	MEAN	2

RCHRES	7	GQUAL	SQAL	5	PLTGEN	11	INPUT	MEAN	3
RCHRES	6	GQUAL	SQAL	5	PLTGEN	11	INPUT	MEAN	4
RCHRES	5	GQUAL	SQAL	5	PLTGEN	11	INPUT	MEAN	5
RCHRES	4	GQUAL	SQAL	5	PLTGEN	11	INPUT	MEAN	6
RCHRES	3	GQUAL	SQAL	5	PLTGEN	11	INPUT	MEAN	7
RCHRES	2	GQUAL	SQAL	5	PLTGEN	11	INPUT	MEAN	8
RCHRES	1	GQUAL	SQAL	5	PLTGEN	11	INPUT	MEAN	9
RCHRES	9	GQUAL	SQAL	6	PLTGEN	12	INPUT	MEAN	1
RCHRES	8	GQUAL	SQAL	6	PLTGEN	12	INPUT	MEAN	2
RCHRES	7	GQUAL	SQAL	6	PLTGEN	12	INPUT	MEAN	3
RCHRES	6	GQUAL	SQAL	6	PLTGEN	12	INPUT	MEAN	4
RCHRES	5	GQUAL	SQAL	6	PLTGEN	12	INPUT	MEAN	5
RCHRES	4	GQUAL	SQAL	6	PLTGEN	12	INPUT	MEAN	6
RCHRES	3	GQUAL	SQAL	6	PLTGEN	12	INPUT	MEAN	7
RCHRES	2	GQUAL	SQAL	6	PLTGEN	12	INPUT	MEAN	8
RCHRES	1	GQUAL	SQAL	6	PLTGEN	12	INPUT	MEAN	9
RCHRES	9	GQUAL	DQAL		PLTGEN	13	INPUT	MEAN	1
RCHRES	8	GQUAL	DQAL		PLTGEN	13	INPUT	MEAN	2
RCHRES	7	GQUAL	DQAL		PLTGEN	13	INPUT	MEAN	3
RCHRES	6	GQUAL	DQAL		PLTGEN	13	INPUT	MEAN	4
RCHRES	5	GQUAL	DQAL		PLTGEN	13	INPUT	MEAN	5
RCHRES	4	GQUAL	DQAL		PLTGEN	13	INPUT	MEAN	6
RCHRES	3	GQUAL	DQAL		PLTGEN	13	INPUT	MEAN	7
RCHRES	2	GQUAL	DQAL		PLTGEN	13	INPUT	MEAN	8
RCHRES	1	GQUAL	DQAL		PLTGEN	13	INPUT	MEAN	9
RCHRES	9	GQUAL	DSQAL	4	PLTGEN	14	INPUT	MEAN	1
RCHRES	8	GQUAL	DSQAL	4	PLTGEN	14	INPUT	MEAN	2
RCHRES	7	GQUAL	DSQAL	4	PLTGEN	14	INPUT	MEAN	3
RCHRES	6	GQUAL	DSQAL	4	PLTGEN	14	INPUT	MEAN	4
RCHRES	5	GQUAL	DSQAL	4	PLTGEN	14	INPUT	MEAN	5
RCHRES	4	GQUAL	DSQAL	4	PLTGEN	14	INPUT	MEAN	6
RCHRES	3	GQUAL	DSQAL	4	PLTGEN	14	INPUT	MEAN	7
RCHRES	2	GQUAL	DSQAL	4	PLTGEN	14	INPUT	MEAN	8
RCHRES	1	GQUAL	DSQAL	4	PLTGEN	14	INPUT	MEAN	9

END NETWORK

MUTSIN

MUTSINFO

<-range><mfl><npt><nmn><nli><mis> ***								
#	-	#	MFL	NPT	NMN	NLI	MSFG	***
01			44	0	09	25	2	
02			45	0	09	25	2	
03			46	0	09	25	2	
20			60	0	08	25	2	

END MUTSINFO

END MUTSIN

PLTGEN

PLOTINFO

#	-	#	FILE	NPT	NMN	LABL	PYR	PIVL	***	-1=monthly; -2=annual;
1			31	0	9	0	12	1		
2			32	0	9	0	12	-2		
3			33	0	9	0	12	24		
4			34	0	9	0	12	1		

5	35	0	9	0	12	-2
6	36	0	9	0	12	1
7	37	0	9	0	12	-2
8	38	0	9	0	12	24
9	51	0	9	0	12	1
10	52	0	9	0	12	1
11	53	0	9	0	12	1
12	54	0	9	0	12	1
13	55	0	9	0	12	1
14	56	0	9	0	12	1

END PLOTINFO

```

GEN-LABELS
# - #<-----Title-----> *** <-----Y axis-
----->
1      Bed Storage
(tons)
2      Bed Depth                                     (ft)
3      Bed Shear Stress
(lb/ft2)
4      TSS Concentration
(mg/l)
5      Outflow
(tons)
6      Deposition or Scour
(tons)
7      Upstream In
(tons)
8      Hourly flow                                     (watershed-
in/hour?)
9      FC concen. in suspended silt                    #/mg
10     FC concen. in suspended clay                     #/mg
11     FC concen. in bed silt                           #/mg
12     FC concen. in bed clay                           #/mg
13     FC concen. in free-phase                         #/l
14     Deposition/Scour of FC                           #/ivld
END GEN-LABELS

```

```

SCALING
# - #      YMIN      YMAX      IVLIN      THRESH ***
1  14      0.        1.E+10     100.
END SCALING

```

```

CURV-DATA      (First curve)
# - #      <-Curve label--> Line Intg  Col Tran ***
# - #      type   eqv  code code ***
1   4      subwatershed 9              AVER
END CURV-DATA
CURV-DATA      (Second curve)
# - #      <-Curve label--> Line Intg  Col Tran ***
# - #      type   eqv  code code ***
1   4      subwatershed 8              AVER
END CURV-DATA

```

```

CURV-DATA          (Third curve)
      <-Curve label--> Line Intg  Col Tran ***
      # - #          type  eqv  code code ***
      1   4    subwatershed 7          AVER
END CURV-DATA
CURV-DATA          (Fourth curve)
      <-Curve label--> Line Intg  Col Tran ***
      # - #          type  eqv  code code ***
      1   4    subwatershed 6          AVER
END CURV-DATA
CURV-DATA          (Fifth curve)
      <-Curve label--> Line Intg  Col Tran ***
      # - #          type  eqv  code code ***
      1   4    subwatershed 5          AVER
END CURV-DATA
CURV-DATA          (Sixth curve)
      <-Curve label--> Line Intg  Col Tran ***
      # - #          type  eqv  code code ***
      1   4    subwatershed 4          AVER
END CURV-DATA
CURV-DATA          <-Curve label--> Line Intg  Col Tran ***
      # - #          type  eqv  code code ***
      1   4    subwatershed 3          AVER
END CURV-DATA
CURV-DATA          <-Curve label--> Line Intg  Col Tran ***
      # - #          type  eqv  code code ***
      1   4    subwatershed 2          AVER
END CURV-DATA
CURV-DATA          <-Curve label--> Line Intg  Col Tran ***
      # - #          type  eqv  code code ***
      1   4    subwatershed 1          AVER
END CURV-DATA
CURV-DATA          <-Curve label--> Line Intg  Col Tran ***
      # - #          type  eqv  code code ***
      5   7    subwatershed 9          SUM
END CURV-DATA
CURV-DATA          (Second curve)
      <-Curve label--> Line Intg  Col Tran ***
      # - #          type  eqv  code code ***
      5   7    subwatershed 8          SUM
END CURV-DATA
CURV-DATA          (Third curve)
      <-Curve label--> Line Intg  Col Tran ***
      # - #          type  eqv  code code ***
      5   7    subwatershed 7          SUM
END CURV-DATA
CURV-DATA          (Fourth curve)
      <-Curve label--> Line Intg  Col Tran ***
      # - #          type  eqv  code code ***
      5   7    subwatershed 6          SUM

```

```

END CURV-DATA
CURV-DATA          (Fifth curve)
    <-Curve label--> Line Intg  Col Tran ***
    # - #          type  eqv  code code ***
    5   7          subwatershed 5      SUM
END CURV-DATA
CURV-DATA          (Sixth curve)
    <-Curve label--> Line Intg  Col Tran ***
    # - #          type  eqv  code code ***
    5   7          subwatershed 4      SUM
END CURV-DATA
CURV-DATA          (Fourth curve)
    <-Curve label--> Line Intg  Col Tran ***
    # - #          type  eqv  code code ***
    5   7          subwatershed 3      SUM
END CURV-DATA
CURV-DATA          (Fifth curve)
    <-Curve label--> Line Intg  Col Tran ***
    # - #          type  eqv  code code ***
    5   7          subwatershed 2      SUM
END CURV-DATA
CURV-DATA          (Sixth curve)
    <-Curve label--> Line Intg  Col Tran ***
    # - #          type  eqv  code code ***
    5   7          subwatershed 1      SUM
END CURV-DATA
CURV-DATA          (First curve)
    <-Curve label--> Line Intg  Col Tran ***
    # - #          type  eqv  code code ***
    8              subwatershed 9      AVER
END CURV-DATA
CURV-DATA          (Second curve)
    <-Curve label--> Line Intg  Col Tran ***
    # - #          type  eqv  code code ***
    8              subwatershed 8      AVER
END CURV-DATA

CURV-DATA          (Third curve)
    <-Curve label--> Line Intg  Col Tran ***
    # - #          type  eqv  code code ***
    8              subwatershed 7      AVER
END CURV-DATA
CURV-DATA          (Fourth curve)
    <-Curve label--> Line Intg  Col Tran ***
    # - #          type  eqv  code code ***
    8              subwatershed 6      AVER
END CURV-DATA
CURV-DATA          (Fifth curve)
    <-Curve label--> Line Intg  Col Tran ***
    # - #          type  eqv  code code ***
    8              subwatershed 5      AVER
END CURV-DATA
CURV-DATA          (Sixth curve)
    <-Curve label--> Line Intg  Col Tran ***

```

```

# - #          type  eqv code code ***
8          subwatershed 4          AVER
END CURV-DATA
CURV-DATA          (Fourth curve)
      <-Curve label--> Line Intg  Col Tran ***
# - #          type  eqv code code ***
8          subwatershed 3          AVER
END CURV-DATA
CURV-DATA          (Fifth curve)
      <-Curve label--> Line Intg  Col Tran ***
# - #          type  eqv code code ***
8          subwatershed 2          AVER
END CURV-DATA
CURV-DATA          (Sixth curve)
      <-Curve label--> Line Intg  Col Tran ***
# - #          type  eqv code code ***
8          subwatershed 1          AVER
END CURV-DATA
CURV-DATA          (First curve)
      <-Curve label--> Line Intg  Col Tran ***
# - #          type  eqv code code ***
9  14          subwatershed 9          AVER
END CURV-DATA
CURV-DATA          (Second curve)
      <-Curve label--> Line Intg  Col Tran ***
# - #          type  eqv code code ***
9  14          subwatershed 8          AVER
END CURV-DATA

CURV-DATA          (Third curve)
      <-Curve label--> Line Intg  Col Tran ***
# - #          type  eqv code code ***
9  14          subwatershed 7          AVER
END CURV-DATA
CURV-DATA          (Fourth curve)
      <-Curve label--> Line Intg  Col Tran ***
# - #          type  eqv code code ***
9  14          subwatershed 6          AVER
END CURV-DATA
CURV-DATA          (Fifth curve)
      <-Curve label--> Line Intg  Col Tran ***
# - #          type  eqv code code ***
9  14          subwatershed 5          AVER
END CURV-DATA
CURV-DATA          (Sixth curve)
      <-Curve label--> Line Intg  Col Tran ***
# - #          type  eqv code code ***
9  14          subwatershed 4          AVER
END CURV-DATA
CURV-DATA          <-Curve label--> Line Intg  Col Tran ***
# - #          type  eqv code code ***
9  14          subwatershed 3          AVER
END CURV-DATA

```

```

CURV-DATA
      <-Curve label--> Line Intg  Col Tran ***
      # - #           type  eqv code code ***
      9   14         subwatershed 2          AVER
END CURV-DATA
CURV-DATA
      <-Curve label--> Line Intg  Col Tran ***
      # - #           type  eqv code code ***
      9   14         subwatershed 1          AVER
END CURV-DATA
END PLTGEN

EXT SOURCES
<-Volume-> <Member> SsysSgap<--Mult-->Tran <-Target vols> <-Grp> <-
Member-> ***
<Name>      x <Name> x tem strg<-factor->strg <Name>      x      x      <Name> x
x ***
WDM3      11 PREC      ENGLZERO      SAME PERLND 101 607 EXTNL PREC
WDM2      13 ATEM      ENGL      SAME PERLND 101 607 EXTNL GATMP
WDM2      17 DEWP      ENGL      SAME PERLND 101 607 EXTNL DTMPG
WDM2      14 WIND      ENGL      SAME PERLND 101 607 EXTNL WINMOV
WDM2      15 SOLR      ENGL      SAME PERLND 101 607 EXTNL SOLRAD
WDM2      16 PEVT      ENGL      SAME PERLND 101 607 EXTNL PETINP
WDM3      11 PREC      ENGLZERO      SAME IMPLND 101      EXTNL PREC
WDM2      13 ATEM      ENGL      SAME IMPLND 101      EXTNL GATMP
WDM2      17 DEWP      ENGL      SAME IMPLND 101      EXTNL DTMPG
WDM2      14 WIND      ENGL      SAME IMPLND 101      EXTNL WINMOV
WDM2      15 SOLR      ENGL      SAME IMPLND 101      EXTNL SOLRAD
WDM2      16 PEVT      ENGL      SAME IMPLND 101      EXTNL PETINP
WDM3      11 PREC      ENGLZERO      SAME RCHRES 1 9 EXTNL PREC
WDM2      13 ATEM      ENGL      SAME RCHRES 1 9 EXTNL GATMP
WDM2      17 DEWP      ENGL      SAME RCHRES 1 9 EXTNL DEWTMP
WDM2      14 WIND      ENGL      SAME RCHRES 1 9 EXTNL WIND
WDM2      15 SOLR      ENGL      SAME RCHRES 1 9 EXTNL SOLRAD
WDM2      18 CLOU      ENGL      SAME RCHRES 1 9 EXTNL CLOUD
WDM2      12 EVAP      ENGL      SAME RCHRES 1 9 EXTNL POTEV
END EXT SOURCES

SCHEMATIC
<-Volume->      <--Area-->      <-Volume->      <ML#> ***
<sb>
<Name>      x      <-factor->      <Name>      x      ***      x
x
PERLND 101      806.55      RCHRES 1 2
PERLND 201      113.73      RCHRES 1 2
PERLND 301      447.2      RCHRES 1 2
PERLND 401      266.02      RCHRES 1 2
PERLND 102      1136.15      RCHRES 2 2
PERLND 202      29.37      RCHRES 2 2
PERLND 302      125.28      RCHRES 2 2
PERLND 402      95.67      RCHRES 2 2
PERLND 103      280.88      RCHRES 3 2
PERLND 203      39.29      RCHRES 3 2
PERLND 303      325.81      RCHRES 3 2

```

PERLND 403	247.12	RCHRES	3	2
PERLND 104	10.95	RCHRES	4	2
PERLND 204	35.7	RCHRES	4	2
PERLND 304	95.92	RCHRES	4	2
PERLND 404	51.4	RCHRES	4	2
PERLND 105	50.5	RCHRES	5	2
PERLND 205	23.72	RCHRES	5	2
PERLND 305	290.17	RCHRES	5	2
PERLND 405	534.23	RCHRES	5	2
PERLND 106	3.54	RCHRES	6	2
PERLND 206	33.63	RCHRES	6	2
PERLND 306	24.01	RCHRES	6	2
PERLND 406	197.27	RCHRES	6	2
PERLND 407	139.63	RCHRES	7	2
PERLND 607	6.86	RCHRES	7	2
PERLND 108	57.21	RCHRES	8	2
PERLND 308	77.28	RCHRES	8	2
PERLND 408	698.21	RCHRES	8	2
PERLND 109	3.71	RCHRES	9	2
PERLND 309	6.37	RCHRES	9	2
PERLND 409	491.81	RCHRES	9	2
IMPLND 101	98.63	RCHRES	1	1
IMPLND 101	27.88	RCHRES	2	1
IMPLND 101	78.69	RCHRES	3	1
IMPLND 101	18.77	RCHRES	4	1
IMPLND 101	351.80	RCHRES	5	1
IMPLND 101	72.96	RCHRES	6	1
IMPLND 101	51.64	RCHRES	7	1
IMPLND 101	258.24	RCHRES	8	1
IMPLND 101	181.90	RCHRES	9	1

*** Reach Connections				***

*** Reach 2 => Reach 1				
RCHRES 2		RCHRES	1	3
*** Reach 3 => Reach 2				
RCHRES 3		RCHRES	2	3
*** Reach 4 => Reach 3				
RCHRES 4		RCHRES	3	3
*** Reach 05 => Reach 4				
RCHRES 5		RCHRES	4	3
*** Reach 06 => Reach 5				
RCHRES 6		RCHRES	5	3
*** Reach 07 => Reach 6				
RCHRES 7		RCHRES	6	3
*** Reach 08 => Reach 7				
RCHRES 8		RCHRES	7	3
*** Reach 09 => Reach 7				
RCHRES 9		RCHRES	7	3
END SCHEMATIC				
MASS-LINK				
MASS-LINK	2			

<-Volume->	<-Grp>	<-Member-><--Mult-->	<-Target vols>	<-Grp>	<-
Member->	***				
<Name>		<Name> x x<-factor->	<Name>		<Name> x
x	***				
PERLND	PWATER	PERO 0.0833333	RCHRES	INFLOW	IVOL
PERLND	SEDMNT	SOSED 1 0.05	RCHRES	INFLOW	ISED 1
PERLND	SEDMNT	SOSED 1 0.60	RCHRES	INFLOW	ISED 2
PERLND	SEDMNT	SOSED 1 0.35	RCHRES	INFLOW	ISED 3
PERLND	PQUAL	POQUAL 1 1.00	RCHRES	INFLOW	IDQAL 1
END MASS-LINK		2			
MASS-LINK		1			
IMPLND	IWATER	SURO 0.0833333	RCHRES	INFLOW	IVOL
IMPLND	SOLIDS	SOSLD 1 0.10	RCHRES	INFLOW	ISED 1
IMPLND	SOLIDS	SOSLD 1 0.50	RCHRES	INFLOW	ISED 2
IMPLND	SOLIDS	SOSLD 1 0.40	RCHRES	INFLOW	ISED 3
IMPLND	IQUAL	SOQUAL 1 1.00	RCHRES	INFLOW	IDQAL 1
END MASS-LINK		1			
MASS-LINK		3			
RCHRES	ROFLOW		RCHRES	INFLOW	
END MASS-LINK		3			
MASS-LINK		4			
RCHRES	ROFLOW	ROVOL	COPY	INPUT	MEAN 1
RCHRES	HYDR	RO	COPY	INPUT	MEAN 2
END MASS-LINK		4			
MASS-LINK		5			
RCHRES	OFLOW	1	RCHRES	INFLOW	
END MASS-LINK		5			
MASS-LINK		6			
RCHRES	OFLOW	2	RCHRES	INFLOW	
END MASS-LINK		6			
END MASS-LINK					
END RUN					

HSPF UCI file for source breakdown:

```
RUN
GLOBAL
  UCI Stroubles Creek Hydrology Calibration
  START      2008/01/01 00:00  END      2013/12/31 24:00
  RUN INTERP OUTPT LEVELS    1    0
  RESUME      0 RUN          1                UNITS      1
END GLOBAL
```

```
FILES
<FILE>  <UN#>***<----FILE NAME----->
----->
MESSU      24    N22_sed.ech
           91    N22_sed.out
           40    WQCalAvg.plt
           41    WQCalMax.plt
           42    WQCalMin.plt
           44    Cattle.mut
           45    Wildlife.mut
           46    Straight_Pipes.mut
           60    ..\N22_Spills.mut
WDM2       26    ..\N22_MET1.wdm
WDM3       27    ..\N22_MET2.wdm
```

END FILES

```
OPN SEQUENCE
  INGRP          INDELT 01:00
    MUTSIN        1
    MUTSIN        2
    MUTSIN        3
    MUTSIN       20
    PERLND       101
    PERLND       201
    PERLND       301
    PERLND       401
    PERLND       102
    PERLND       202
    PERLND       302
    PERLND       402
    PERLND       103
    PERLND       203
    PERLND       303
    PERLND       403
    PERLND       104
    PERLND       204
    PERLND       304
    PERLND       404
    PERLND       105
    PERLND       205
    PERLND       305
    PERLND       405
    PERLND       106
```

```

PERLND      206
PERLND      306
PERLND      406
PERLND      407
PERLND      607
PERLND      108
PERLND      308
PERLND      408
PERLND      109
PERLND      309
PERLND      409
IMPLND      101
RCHRES       9
RCHRES       8
RCHRES       7
RCHRES       6
RCHRES       5
RCHRES       4
RCHRES       3
RCHRES       2
RCHRES       1
GENER        1
GENER        2
GENER        3
GENER        4
GENER        5
GENER        6
GENER        7
GENER        8
PLTGEN       1
PLTGEN       2
PLTGEN       3

```

```

END INGRP
END OPN SEQUENCE

```

```

PERLND

```

```

ACTIVITY

```

```

*** <PLS > Active Sections ***
*** x - x ATMP SNOW PWAT SED PST PWG PQAL MSTL PEST NITR PHOS TRAC ***
101 607 0 0 1 0 0 0 1 0 0 0 0 0
END ACTIVITY

```

```

PRINT-INFO

```

```

*** < PLS> Print-flags
PIVL PYR
*** x - x ATMP SNOW PWAT SED PST PWG PQAL MSTL PEST NITR PHOS TRAC
101 607 4 4 4 4 4 4 4 4 4 4 4
1 12
END PRINT-INFO

```

```

GEN-INFO

```

```

*** Name Unit-systems Printer BinaryOut
*** <PLS > t-series Engl Metr Engl Metr

```

```

*** x - x
101 Forest -1 1 1 0 0 0 0
201 Cropland-1 1 1 0 0 0 0
301 Pasture-1 1 1 0 0 0 0
401 Residential-1 1 1 0 0 0 0
102 Forest-2 1 1 0 0 0 0
202 Cropland-2 1 1 0 0 0 0
302 Pasture-2 1 1 0 0 0 0
402 Residential-2 1 1 0 0 0 0
103 Forest-3 1 1 0 0 0 0
203 Cropland-3 1 1 0 0 0 0
303 Pasture-3 1 1 0 0 0 0
403 Residential-3 1 1 0 0 0 0
104 Forest-4 1 1 0 0 0 0
204 Cropland-4 1 1 0 0 0 0
304 Pasture-4 1 1 0 0 0 0
404 Residential-4 1 1 0 0 0 0
105 Forest-5 1 1 0 0 0 0
205 Cropland-5 1 1 0 0 0 0
305 Pasture-5 1 1 0 0 0 0
405 Residential-5 1 1 0 0 0 0
106 Forest-6 1 1 0 0 0 0
206 Cropland-6 1 1 0 0 0 0
306 Pasture-6 1 1 0 0 0 0
406 Residential-6 1 1 0 0 0 0
407 Residential-7 1 1 0 0 0 0
607 Water-7 1 1 0 0 0 0
108 Forest-8 1 1 0 0 0 0
308 Pasture-8 1 1 0 0 0 0
408 Residential-8 1 1 0 0 0 0
109 Forest-9 1 1 0 0 0 0
309 Pasture-9 1 1 0 0 0 0
409 Residential-9 1 1 0 0 0 0
END GEN-INFO

```

```

PWAT-PARM1
*** <PLS >
Flags
*** x - x CSNO RTOP UZFG VCS VUZ VNN VIFW VIRG VLE IFFC HWT IRRG
101 607 0 1 1 1 1 0 0 0 1 0 0 0
END PWAT-PARM1

```

```

PWAT-PARM2
*** < PLS> FOREST LZSN INFILT LSUR SLSUR KVARV
AGWRC
*** x - x (in) (in/hr) (ft) (1/in)
(1/day)
101 1. 15.0 0.357 124.2 0.107 0.1
0.990
102 1. 15.0 0.358 132.6 0.108 0.1
0.990
103 1. 15.0 0.373 133.1 0.123 0.1
0.990
104 1. 15.0 0.36 238.1 0.11 0.1
0.990

```

105	1.	15.0	0.368	164.3	0.118	0.1
0.990						
106	1.	15.0	0.342	121.1	0.092	0.1
0.990						
108	1.	15.0	0.318	189.9	0.068	0.1
0.990						
109	1.	15.0	0.337	234.3	0.087	0.1
0.990						
201	0.	12.0	0.268	141.8	0.118	0.1
0.990						
202	0.	12.0	0.297	122.5	0.147	0.1
0.990						
203	0.	12.0	0.274	184.1	0.124	0.1
0.990						
204	0.	12.0	0.32	206.4	0.17	0.1
0.990						
205	0.	12.0	0.312	198.2	0.162	0.1
0.990						
206	0.	12.0	0.252	247.3	0.102	0.1
0.990						
301	0.	12.0	0.267	123.9	0.117	0.1
0.990						
302	0.	12.0	0.301	130.6	0.151	0.1
0.990						
303	0.	12.0	0.286	111.1	0.136	0.1
0.990						
304	0.	12.0	0.316	145.1	0.166	0.1
0.990						
305	0.	12.0	0.307	143.7	0.157	0.1
0.990						
306	0.	12.0	0.329	125.9	0.179	0.1
0.990						
308	0.	12.0	0.222	176.8	0.072	0.1
0.990						
309	0.	12.0	0.276	148.3	0.126	0.1
0.990						
401	0.	10.0	0.254	137.5	0.124	0.1
0.966						
402	0.	10.0	0.26	132.5	0.13	0.1
0.966						
403	0.	10.0	0.256	139.4	0.126	0.1
0.966						
404	0.	10.0	0.255	156.7	0.125	0.1
0.966						
405	0.	10.0	0.248	146.2	0.118	0.1
0.966						
406	0.	10.0	0.234	147.6	0.104	0.1
0.966						
407	0.	10.0	0.209	143.6	0.079	0.1
0.966						
408	0.	10.0	0.204	153.2	0.074	0.1
0.966						
409	0.	10.0	0.221	151.0	0.091	0.1
0.966						

```

        607          0.          10.0        0.500          143        0.100          0.1
0.966
END PWAT-PARM2

```

```

PWAT-PARM3
*** < PLS>      PETMAX      PETMIN      INFEXP      INFILD      DEEPFR      BASETP
AGWETP
*** x  -  x      (deg F)      (deg F)
    101  607      40.          35.          2.          2.          0.29          0.030
0.00
END PWAT-PARM3

```

```

PWAT-PARM4
*** <PLS >      CEPSC      UZSN      NSUR      INTFW      IRC      LZETP
*** x  -  x      (in)      (in)      (1/day)
    101  109      0.20      1.00      0.50      5.0      0.90      0.6
    201  206      0.10      1.00      0.35      5.0      0.90      0.4
    301  309      0.10      1.00      0.35      5.0      0.90      0.3
    401  409      0.05      1.00      0.20      5.0      0.90      0.2
    607          0.00      1.00      0.35      5.0      0.90      0.2
END PWAT-PARM4

```

```

PWAT-STATE1
*** < PLS> PWATER state variables (in)
*** x  -  x      CEPS      SURS      UZS      IFWS      LZS      AGWS
GWVS
    101  607      0.0      0.00      0.9      0.00      9.4      1
0.00
END PWAT-STATE1

```

```

MON-INTERCEP
*** <PLS > Interception storage capacity at start of each month (in)
*** x  -  x  JAN  FEB  MAR  APR  MAY  JUN  JUL  AUG  SEP  OCT  NOV  DEC
    101  109  0.20  0.20  0.20  0.20  0.20  0.20  0.20  0.20  0.20  0.20  0.20  0.20
    201  206  0.20  0.20  0.20  0.20  0.20  0.22  0.22  0.22  0.20  0.20  0.20  0.20
    301  309  0.15  0.15  0.15  0.15  0.15  0.16  0.16  0.16  0.16  0.16  0.16  0.16
    401  409  0.05  0.05  0.05  0.05  0.05  0.05  0.05  0.05  0.05  0.05  0.05  0.05
    607          0.01  0.01  0.01  0.01  0.01  0.01  0.01  0.01  0.01  0.01  0.01  0.01
END MON-INTERCEP

```

```

MON-UZSN
*** <PLS > Upper zone storage at start of each month (inches)
*** x  -  x  JAN  FEB  MAR  APR  MAY  JUN  JUL  AUG  SEP  OCT  NOV  DEC
    101  109  1.10  1.10  1.10  1.00  1.00  1.00  1.00  1.00  1.00  1.10  1.10  1.10
    201  206  1.10  1.10  1.10  1.00  1.00  1.00  1.00  1.00  1.00  1.10  1.10  1.10
    301  309  1.10  1.10  1.10  1.00  1.00  1.00  1.00  1.00  1.00  1.10  1.10  1.10
    401  409  1.10  1.10  1.10  1.00  1.00  1.00  1.00  1.00  1.00  1.10  1.10  1.10
    607          1.10  1.10  1.10  1.00  1.00  1.00  1.00  1.00  1.00  1.10  1.10  1.10
END MON-UZSN

```

```

MON-LZETPARM
*** <PLS > Lower zone evapotransp parm at start of each month
*** x  -  x  JAN  FEB  MAR  APR  MAY  JUN  JUL  AUG  SEP  OCT  NOV  DEC
    101  109  0.65  0.65  0.65  0.65  0.65  0.66  0.66  0.66  0.65  0.65  0.65  0.65

```

```

201 206 0.40 0.40 0.40 0.40 0.40 0.40 0.40 0.40 0.40 0.40 0.40 0.40
301 309 0.40 0.40 0.40 0.40 0.40 0.40 0.40 0.40 0.40 0.40 0.40 0.40
401 409 0.20 0.20 0.20 0.20 0.20 0.20 0.20 0.20 0.20 0.20 0.20 0.20
607      0.20 0.20 0.20 0.20 0.20 0.20 0.20 0.20 0.20 0.20 0.20 0.20
END MON-LZETPARM

```

*** section GQUAL (for fecal indicator bacteria)

```

NQUALS
#      #NQUAL ***
101 607      4
END NQUALS

```

QUAL-PROPS

*** <PLS > Identifiers and Flags

```

*** x - x      QUALID      QTID  QSD  VPFW  VPFS  QSO  VQO  QIFW  VIQC  QAGW
VAQC
101 607FC livestock      #      0      0      0      1      1      1      0      1
0
END QUAL-PROPS

```

QUAL-INPUT

```

***          SQO  POTFW  POTFS  ACQOP  SQOLIM  WSQOP  IOQC  AOQC
*** <PLS >  qty/ac qty/ton qty/ton  qty/  qty/ac  in/hr  qty/ft3 qty/ft3
*** x - x          ac.day
101 109 0E+10      0.      0.  1E+10  9E+10  2.00  177.  118.
201 203 0E+10      0.      0.  1E+10  9E+10  0.20  531.  354.
204 206 0E+10      0.      0.  1E+10  9E+10  0.10  531.  354.
301 303 0E+10      0.      0.  1E+10  9E+10  0.20  177.  118.
304 309 0E+10      0.      0.  1E+10  9E+10  0.10  177.  118.
401 403 0E+10      0.      0.  1E+10  9E+10  0.10  531.  354.
404 409 0E+10      0.      0.  1E+10  9E+10  0.01  531.  354.
607      0E+10      0.      0.  1E+10  9E+10  0.10  531.  354.
END QUAL-INPUT

```

MON-POTFW

```

#      #  JAN  FEB  MAR  APR  MAY  JUN  JUL  AUG  SEP  OCT  NOV  DEC
***
101 109 .030 .010 .180 .060 .120 .302 .201 .804 .400 .120 .240 .015
201 209 2.55 0.43 0.50 1.59 3.17 4.75 3.17 2.66 3.17 3.17 2.66 1.28
301 309 2.55 0.43 0.50 1.59 3.17 4.75 3.17 2.66 3.17 3.17 2.66 1.28
401 409 .21  .28  .48 1.28 2.57 1.93 2.57 5.14 0.28 1.24 1.24  .42
607
END MON-POTFW

```

MON-ACCUM

*** <PLS > Value at start of each month for accum rate of QUALOF
 (#/ac.day)

```

*** x - x  JAN  FEB  MAR  APR  MAY  JUN  JUL  AUG  SEP  OCT  NOV  DEC
*** N22-1
201      0E+000E+0010E0711E0710E070E+000E+000E+000E+0019E0619E060E+00
301      14E0715E0715E0716E0716E0716E0716E0717E0717E0713E0713E0713E07
401      0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
101      0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00

```

```

*** N22-2
202 0E+000E+0030E0533E0532E050E+000E+000E+000E+0057E0456E040E+00
302 0E+000E+0020E0522E0521E050E+000E+000E+0022E0521E0520E050E+00
402 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
102 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
*** N22-3
203 0E+000E+0015E0816E0815E080E+000E+000E+000E+0028E0729E070E+00
303 14E0916E0916E0916E0917E0917E0917E0918E0918E0913E0913E0913E09
403 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
103 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
*** N22-4
204 0E+000E+0025E0726E0725E070E+000E+000E+000E+0046E0648E060E+00
304 38E0842E0843E0843E0844E0845E0846E0846E0847E0835E0836E0837E08
404 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
104 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
*** N22-5
205 0E+000E+0011E0811E0811E080E+000E+000E+000E+0020E0720E070E+00
305 83E0893E0897E0899E0810E0910E0911E0911E0911E0977E0880E0880E08
405 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
105 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
*** N22-6
206 0E+000E+0080E0783E0780E070E+000E+000E+000E+0015E0715E070E+00
306 11E1012E1013E1013E1013E1013E1014E1014E1014E1099E0910E1011E10
406 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
106 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
*** N22-7
407 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
*** N22-8
308 0E+000E+0020E0522E0521E050E+000E+000E+0022E0521E0520E050E+00
408 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
108 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
*** N22-9
309 0E+000E+0020E0522E0521E050E+000E+000E+0022E0521E0520E050E+00
409 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
109 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
END MON-ACCUM

```

MON-SQOLIM

```

*** <PLS > Value at start of month for limiting storage of QUALOF (#/ac)
*** x - x JAN FEB MAR APR MAY JUN JUL AUG SEP OCT NOV DEC
*** N22-1
201 1E-011E-0193E0796E0793E071E-011E-011E-011E-0117E0717E071E-01
301 12E0814E0814E0814E0814E0815E0815E0815E0815E0811E0812E0812E08
401 1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
101 1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
*** N22-2
202 1E-011E-0127E0629E0628E061E-011E-011E-011E-0152E0550E051E-01
302 1E-011E-0118E0620E0619E061E-011E-011E-0120E0619E0618E061E-01
402 1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
102 1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
*** N22-3
203 1E-011E-0114E0914E0914E091E-011E-011E-011E-0125E0826E081E-01
303 12E1014E1014E1015E1015E1015E1016E1016E1016E1011E1012E1012E10
403 1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01

```

```

103      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
*** N22-4
204      1E-011E-0123E0824E0823E081E-011E-011E-011E-0141E0743E071E-01
304      34E0937E0938E0939E0940E0940E0941E0942E0943E0932E0932E0933E09
404      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
104      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
*** N22-5
205      1E-011E-0198E0810E0998E081E-011E-011E-011E-0118E0818E081E-01
305      75E0984E0988E0990E0991E0993E0995E0996E0999E0969E0972E0972E09
405      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
105      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
*** N22-6
206      1E-011E-0172E0874E0872E081E-011E-011E-011E-0113E0814E081E-01
306      99E1011E1111E1112E1112E1112E1112E1113E1113E1189E1093E1096E10
406      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
106      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
*** N22-7
407      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
*** N22-8
308      1E-011E-0118E0620E0619E061E-011E-011E-0120E0619E0618E061E-01
408      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
108      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
*** N22-9
309      1E-011E-0118E0620E0619E061E-011E-011E-0120E0619E0618E061E-01
409      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
109      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
END MON-SQOLIM

```

QUAL-PROPS

```

*** <PLS > Identifiers and Flags
*** x - x      QUALID      QTID  QSD  VPFW  VPFS   QSO   VQO  QIFW  VIQC  QAGW
VAQC
101  607FC pet          #          0    0    0    1    1    1    0    1
0
END QUAL-PROPS

```

QUAL-INPUT

```

***          SQO   POTFW   POTFS   ACQOP   SQOLIM   WSQOP   IOQC   AOQC
*** <PLS >  qty/ac qty/ton qty/ton  qty/   qty/ac   in/hr  qty/ft3 qty/ft3
*** x - x          ac.day
101  109   0E+10    0.    0.   1E+10   9E+10   2.00   177.   118.
201  203   0E+10    0.    0.   1E+10   9E+10   0.20   531.   354.
204  206   0E+10    0.    0.   1E+10   9E+10   0.10   531.   354.
301  303   0E+10    0.    0.   1E+10   9E+10   0.20   177.   118.
304  309   0E+10    0.    0.   1E+10   9E+10   0.10   177.   118.
401  403   0E+10    0.    0.   1E+10   9E+10   0.10   531.   354.
404  409   0E+10    0.    0.   1E+10   9E+10   0.01   531.   354.
607          0E+10    0.    0.   1E+10   9E+10   0.10   531.   354.
END QUAL-INPUT

```

MON-ACCUM

```

*** <PLS > Value at start of each month for accum rate of QUALOF
(#/ac.day)
*** x - x      JAN   FEB   MAR   APR   MAY   JUN   JUL   AUG   SEP   OCT   NOV   DEC

```

```

*** N22-1
201 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
301 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
401 38E0738E0738E0738E0738E0738E0738E0738E0738E0738E0738E07
101 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
*** N22-2
202 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
302 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
402 37E0737E0737E0737E0737E0737E0737E0737E0737E0737E0737E07
102 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
*** N22-3
203 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
303 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
403 24E0724E0724E0724E0724E0724E0724E0724E0724E0724E0724E07
103 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
*** N22-4
204 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
304 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
404 42E0742E0742E0742E0742E0742E0742E0742E0742E0742E0742E07
104 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
*** N22-5
205 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
305 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
405 11E0811E0811E0811E0811E0811E0811E0811E0811E0811E0811E08
105 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
*** N22-6
206 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
306 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
406 62E0662E0662E0662E0662E0662E0662E0662E0662E0662E0662E06
106 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
*** N22-7
407 16E0716E0716E0716E0716E0716E0716E0716E0716E0716E0716E07
*** N22-8
308 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
408 17E0817E0817E0817E0817E0817E0817E0817E0817E0817E0817E08
108 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
*** N22-9
309 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
409 32E0832E0832E0832E0832E0832E0832E0832E0832E0832E0832E08
109 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
END MON-ACCUM

```

MON-SQOLIM

```

*** <PLS > Value at start of month for limiting storage of QUALOF
(#/ac)END PERLND
*** x - x JAN FEB MAR APR MAY JUN JUL AUG SEP OCT NOV DEC
*** N22-1
201 1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
301 1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
401 35E0835E0835E0835E0835E0835E0835E0835E0835E0835E0835E08
101 1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
*** N22-2
202 1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
302 1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01

```

```

402      33E0833E0833E0833E0833E0833E0833E0833E0833E0833E0833E0833E08
102      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
*** N22-3
203      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
303      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
403      21E0821E0821E0821E0821E0821E0821E0821E0821E0821E0821E0821E08
103      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
*** N22-4
204      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
304      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
404      38E0838E0838E0838E0838E0838E0838E0838E0838E0838E0838E0838E08
104      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
*** N22-5
205      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
305      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
405      97E0897E0897E0897E0897E0897E0897E0897E0897E0897E0897E0897E08
105      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
*** N22-6
206      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
306      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
406      56E0756E0756E0756E0756E0756E0756E0756E0756E0756E0756E0756E07
106      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
*** N22-7
407      14E0814E0814E0814E0814E0814E0814E0814E0814E0814E0814E0814E08
*** N22-8
308      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
408      16E0916E0916E0916E0916E0916E0916E0916E0916E0916E0916E0916E09
108      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
*** N22-9
309      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
409      29E0929E0929E0929E0929E0929E0929E0929E0929E0929E0929E0929E09
109      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
END MON-SQOLIM

```

QUAL-PROPS

```

*** <PLS > Identifiers and Flags
*** x - x      QUALID      QTID  QSD  VPFW  VPFS   QSO   VQO  QIFW  VIQC  QAGW
VAQC
101  607FC Septic      #          0    0    0    1    1    1    0    1
0
END QUAL-PROPS

```

QUAL-INPUT

```

***          SQO    POTFW    POTFS    ACQOP    SQOLIM    WSQOP    IOQC    AOQC
*** <PLS >  qty/ac  qty/ton  qty/ton    qty/    qty/ac    in/hr  qty/ft3  qty/ft3
*** x - x          ac.day
101  109    0E+10     0.      0.    1E+10    9E+10    2.00    177.    118.
201  203    0E+10     0.      0.    1E+10    9E+10    0.20    531.    354.
204  206    0E+10     0.      0.    1E+10    9E+10    0.10    531.    354.
301  303    0E+10     0.      0.    1E+10    9E+10    0.20    177.    118.
304  309    0E+10     0.      0.    1E+10    9E+10    0.10    177.    118.
401  403    0E+10     0.      0.    1E+10    9E+10    0.10    531.    354.
404  409    0E+10     0.      0.    1E+10    9E+10    0.01    531.    354.
607          0E+10     0.      0.    1E+10    9E+10    0.10    531.    354.

```

END QUAL-INPUT

MON-ACCUM

*** <PLS > Value at start of each month for accum rate of QUALOF
(#/ac.day)

*** x - x JAN FEB MAR APR MAY JUN JUL AUG SEP OCT NOV DEC

*** N22-1

201 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
301 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
401 13E0713E0713E0713E0713E0713E0713E0713E0713E0713E0713E07
101 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00

*** N22-2

202 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
302 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
402 30E0730E0730E0730E0730E0730E0730E0730E0730E0730E0730E07
102 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00

*** N22-3

203 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
303 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
403 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
103 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00

*** N22-4

204 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
304 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
404 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
104 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00

*** N22-5

205 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
305 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
405 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
105 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00

*** N22-6

206 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
306 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
406 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
106 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00

*** N22-7

407 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00

*** N22-8

308 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
408 67E0567E0567E0567E0567E0567E0567E0567E0567E0567E0567E05
108 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00

*** N22-9

309 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
409 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00
109 0E+000E+000E+000E+000E+000E+000E+000E+000E+000E+000E+00

END MON-ACCUM

MON-SQOLIM

*** <PLS > Value at start of month for limiting storage of QUALOF (#/ac)

*** x - x JAN FEB MAR APR MAY JUN JUL AUG SEP OCT NOV DEC

*** N22-1

201 1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
301 1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01

```

401      11E0811E0811E0811E0811E0811E0811E0811E0811E0811E0811E0811E08
101      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
*** N22-2
202      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
302      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
402      27E0827E0827E0827E0827E0827E0827E0827E0827E0827E0827E08
102      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
*** N22-3
203      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
303      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
403      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
103      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
*** N22-4
204      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
304      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
404      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
104      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
*** N22-5
205      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
305      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
405      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
105      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
*** N22-6
206      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
306      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
406      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
106      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
*** N22-7
407      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
*** N22-8
308      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
408      61E0661E0661E0661E0661E0661E0661E0661E0661E0661E0661E06
108      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
*** N22-9
309      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
409      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
109      1E-011E-011E-011E-011E-011E-011E-011E-011E-011E-011E-01
END MON-SQOLIM
QUAL-PROPS
*** <PLS >  Identifiers and Flags
*** x - x      QUALID      QTID  QSD VPFW VPFS   QSO   VQO QIFW VIQC QAGW
VAQC
101  607FC wildlife      #          0    0    0    1    1    1    0    1
0
END QUAL-PROPS

QUAL-INPUT
***          SQO   POTFW   POTFS   ACQOP   SQOLIM   WSQOP   IOQC   AOQC
*** <PLS >  qty/ac qty/ton qty/ton   qty/   qty/ac   in/hr  qty/ft3 qty/ft3
*** x - x          ac.day
101  109    0E+10     0.     0.    1E+10    9E+10    2.00    177.    118.
201  203    0E+10     0.     0.    1E+10    9E+10    0.20    531.    354.
204  206    0E+10     0.     0.    1E+10    9E+10    0.10    531.    354.
301  303    0E+10     0.     0.    1E+10    9E+10    0.20    177.    118.

```



```

*** x - x JAN FEB MAR APR MAY JUN JUL AUG SEP OCT NOV DEC
*** N22-1
201 11E0711E0711E0711E0711E0711E0711E0711E0711E0711E0711E07
301 11E0711E0711E0711E0711E0711E0711E0711E0711E0711E0711E07
401 17E0717E0717E0717E0717E0717E0717E0717E0717E0717E0717E07
101 11E0711E0711E0711E0711E0711E0711E0711E0711E0711E0711E07
*** N22-2
202 54E0654E0654E0654E0654E0654E0654E0654E0654E0654E0654E06
302 54E0654E0654E0654E0654E0654E0654E0654E0654E0654E0654E06
402 83E0683E0683E0683E0683E0683E0683E0683E0683E0683E0683E06
102 59E0659E0659E0659E0659E0659E0659E0659E0659E0659E0659E06
*** N22-3
203 14E0714E0714E0714E0714E0714E0714E0714E0714E0714E0714E07
303 14E0714E0714E0714E0714E0714E0714E0714E0714E0714E0714E07
403 22E0722E0722E0722E0722E0722E0722E0722E0722E0722E0722E07
103 15E0715E0715E0715E0715E0715E0715E0715E0715E0715E0715E07
*** N22-4
204 26E0726E0726E0726E0726E0726E0726E0726E0726E0726E0726E07
304 26E0726E0726E0726E0726E0726E0726E0726E0726E0726E0726E07
404 42E0742E0742E0742E0742E0742E0742E0742E0742E0742E0742E07
104 30E0730E0730E0730E0730E0730E0730E0730E0730E0730E0730E07
*** N22-5
205 18E0718E0718E0718E0718E0718E0718E0718E0718E0718E0718E07
305 18E0718E0718E0718E0718E0718E0718E0718E0718E0718E0718E07
405 28E0728E0728E0728E0728E0728E0728E0728E0728E0728E0728E07
105 20E0720E0720E0720E0720E0720E0720E0720E0720E0720E0720E07
*** N22-6
206 41E0741E0741E0741E0741E0741E0741E0741E0741E0741E0741E07
306 41E0741E0741E0741E0741E0741E0741E0741E0741E0741E0741E07
406 65E0765E0765E0765E0765E0765E0765E0765E0765E0765E0765E07
106 41E0741E0741E0741E0741E0741E0741E0741E0741E0741E0741E07
*** N22-7
407 39E0839E0839E0839E0839E0839E0839E0839E0839E0839E0839E08
*** N22-8
308 38E0738E0738E0738E0738E0738E0738E0738E0738E0738E0738E07
408 55E0755E0755E0755E0755E0755E0755E0755E0755E0755E0755E07
108 41E0741E0741E0741E0741E0741E0741E0741E0741E0741E0741E07
*** N22-9
309 59E0759E0759E0759E0759E0759E0759E0759E0759E0759E0759E07
409 55E0755E0755E0755E0755E0755E0755E0755E0755E0755E0755E07
109 11E0811E0811E0811E0811E0811E0811E0811E0811E0811E0811E08
END MON-SQOLIM
END PERLND

```

IMPLND

```

ACTIVITY
*** <ILS > Active Sections
*** x - x ATMP SNOW IWAT SLD IWG IQAL
101 0 0 1 0 0 1
END ACTIVITY

```

GEN-INFO

```

*** Name Unit-systems Printer BinaryOut
*** <ILS > t-series Engl Metr Engl Metr

```

```

*** x - x                               in  out
101                                     1   1   0   0   0   0
END GEN-INFO

```

```

IWAT-PARM1
*** <ILS >           Flags
*** x - x CSNO RTOP  VRS  VNN RTLI
101         0    1    0    0    0
END IWAT-PARM1

```

```

IWAT-PARM2
*** <ILS >           LSUR           SLSUR           NSUR           RETSC
*** x - x           (ft)           (in)
101 106           100.           0.150           0.10           0.150
107           100.           0.150           0.10           0.300
108 109           100.           0.150           0.10           0.250
END IWAT-PARM2

```

```

IWAT-PARM3
*** <ILS >           PETMAX           PETMIN
*** x - x           (deg F)           (deg F)
101           40.           35.
END IWAT-PARM3

```

```

IWAT-STATE1
*** <ILS > IWATER state variables (inches)
*** x - x           RETS           SURS
101           0.0           0.00
END IWAT-STATE1

```

```

QUAL-PROPS
*** <ILS >
*** x - x           QUALID           QTID           QSD VPFW           QSO           VQO
101           FC           #           0           0           1           0
END QUAL-PROPS

```

```

QUAL-INPUT
***           Storage on surface and nonseasonal parameters
***           SQO           POTFW           ACQOP           SQOLIM           WSQOP
*** <ILS > qty/ac qty/ton           qty/           qty/ac           in/hr
*** x - x           ac.day
101           1E+07           0.           1E+07           3E+07           0.01
END QUAL-INPUT
END IMPLND

```

```

RCHRES
ACTIVITY
*** RCHRES Active sections
*** x - x HYFG ADFG CNFG HTFG SDFG GQFG OXFG NUFG PKFG PHFG
1    9    1    1    0    0    0    1    0    0    0    0
END ACTIVITY

```

```

GEN-INFO
***           Name           Nexits           Unit Systems           Printer

```

```

*** RCHRES                               t-series  Engr Metr LKFG
*** x - x                               in  out
    1    9  StroublesCrk                1    1    0    0    0    0
0
END GEN-INFO

HYDR-PARM1
***          Flags for HYDR section
***RC HRES  VC A1 A2 A3  ODFVFG for each *** ODGTFG for each      FUNCT
for each
*** x - x  FG FG FG FG  possible  exit *** possible  exit      possible
exit
    1    9    0  1  1  1    4  0  0  0  0    0  0  0  0  0    1  1  1
1  1
END HYDR-PARM1

HYDR-PARM2
*** RCHRES FTBW FTBU          LEN          DELTH          STCOR          KS          DB50
*** x - x          (miles)          (ft)          (ft)          KS          (in)
    1          0.    1    2.29    119.7    3.2    0.5    0.2
    2          0.    2    2.41    62.91    3.2    0.5    0.2
    3          0.    3    0.49     6.7    3.2    0.5    0.2
    4          0.    4    0.54     7.17    3.2    0.5    0.2
    5          0.    5    0.80    16.28    3.2    0.5    0.2
    6          0.    6    0.62    17.07    3.2    0.5    0.2
    7          0.    7    0.28     7.87    3.2    0.5    0.2
    8          0.    8    1.30    90.65    3.2    0.5    0.2
    9          0.    9    1.78    173.9    3.2    0.5    0.2
END HYDR-PARM2

MON-CONVF
*** RCHRES  Monthly f(VOL) adjustment factors
*** x - x  JAN  FEB  MAR  APR  MAY  JUN  JUL  AUG  SEP  OCT  NOV  DEC
    1    9 0.90 0.89 0.89 0.91 0.93 1.99 1.99 1.99 0.99 0.98 0.98 0.90
END MON-CONVF

HYDR-INIT
***          Initial conditions for HYDR section
*** RCHRES          VOL  CAT Initial value of COLIND          initial value of
OUTDGT
*** x - x          ac-ft          for each possible  exit  for each possible
exit,ft3
    1    9          10.0          4.2  4.5  4.5  4.5  4.2          2.1  1.2  0.5
1.2  1.8
END HYDR-INIT

***FIB section*****

ADCALC-DATA
*** RCHRES
*** x - x          CRRAT          VOL
    1    9          1.5          100
END ADCALC-DATA

```

```

GQ-GENDATA
*** RCHRES
*** x - x NGQL TPGF PHFG ROFG CDFG SDFG PYFG LAT
      1   9   4   2   2   2   2   2   2   2
END GQ-GENDATA

GQ-QALDATA
*** RCHRES          GQID      DQAL      CONCID      CONV      QTYID
*** x - x          concid
      1   9FC      100.      #/10      0.0035  #
END GQ-QALDATA
GQ-QALDATA
*** RCHRES          GQID      DQAL      CONCID      CONV      QTYID
*** x - x          concid
      1   9FC      100.      #/10      0.0035  #
END GQ-QALDATA
GQ-QALDATA
*** RCHRES          GQID      DQAL      CONCID      CONV      QTYID
*** x - x          concid
      1   9FC      100.      #/10      0.0035  #
END GQ-QALDATA
GQ-QALDATA
*** RCHRES          GQID      DQAL      CONCID      CONV      QTYID
*** x - x          concid
      1   9FC      100.      #/10      0.0035  #
END GQ-QALDATA

GQ-QALFG
*** RCHRES HDRL OXID PHOT VOLT BIOD  GEN SDAS
*** x - x
      1   9   0   0   0   0   0   1   0
END GQ-QALFG
GQ-QALFG
*** RCHRES HDRL OXID PHOT VOLT BIOD  GEN SDAS
*** x - x
      1   9   0   0   0   0   0   1   0
END GQ-QALFG
GQ-QALFG
*** RCHRES HDRL OXID PHOT VOLT BIOD  GEN SDAS
*** x - x
      1   9   0   0   0   0   0   1   0
END GQ-QALFG
GQ-QALFG
*** RCHRES HDRL OXID PHOT VOLT BIOD  GEN SDAS
*** x - x
      1   9   0   0   0   0   0   1   0
END GQ-QALFG

GQ-GENDECAY
*** RCHRES      FSTDEC      THFST
*** x - x      (/day)
      1   3      1.15      1.05
      7      4.00      1.05
      4   9      1.15      1.05
END GQ-GENDECAY

```

```

GQ-GENDECAY
*** RCHRES      FSTDEC      THFST
*** x - x      (/day)
    1    3      1.15      1.05
    7          4.00      1.05
    4    9      1.15      1.05
END GQ-GENDECAY
GQ-GENDECAY
*** RCHRES      FSTDEC      THFST
*** x - x      (/day)
    1    3      1.15      1.05
    7          4.00      1.05
    4    9      1.15      1.05
END GQ-GENDECAY
GQ-GENDECAY
*** RCHRES      FSTDEC      THFST
*** x - x      (/day)
    1    3      1.15      1.05
    7          4.00      1.05
    4    9      1.15      1.05
END GQ-GENDECAY
END RCHRES

FTABLES
FTABLE      1
rows cols
4    4
depth      area      volume      outflow1 ***
0.         5.22      0.         0.
0.01      5.22      0.05      0.
2.93      11.55     24.61     476.35
45.59     601.48    1773.82    169167.
END FTABLE 1

FTABLE      2
rows cols
4    4
depth      area      volume      outflow1 ***
0.         19.43     0.         0.
0.01      19.43     0.19      0.
1.9        19.2     36.68     252.84
83.92     437.52    25063.55  1006730.09
END FTABLE 2

FTABLE      3
rows cols
4    4
depth      area      volume      outflow1 ***
0.         3.38      0.         0.
0.01      3.38      0.03      0.
1.76      3.34      5.9       203.87
28.        47.32     853.68    64940.09
END FTABLE 3

```

```

FTABLE      4
rows cols
  4      4
    depth      area      volume      outflow1 ***
      0.        3.59        0.        0.
     0.01       3.59       0.04        0.
     1.66       3.54       5.92       174.8
    25.28      71.51     901.73    44353.9
END FTABLE  4

FTABLE      5
rows cols
  4      4
    depth      area      volume      outflow1 ***
      0.        5.12        0.        0.
     0.01       5.12       0.05        0.
     1.63       5.05       8.3       166.84
    11.48     95.09     569.86   13866.32
END FTABLE  5

FTABLE      6
rows cols
  4      4
    depth      area      volume      outflow1 ***
      0.        3.38        0.        0.
     0.01       3.38       0.03        0.
     1.44       3.32       4.83       118.21
    11.61    143.71     940.84   22476.73
END FTABLE  6

FTABLE      7
rows cols
  7      4
    depth      area      volume      outflow1 ***
*** (feet) (acres) (ac-ft) (cfs)
      0.        0.00        0.        0.
     1.46       1.82     2.2568     0.405
     2.92       3.82     6.2568     0.567
     6.84       4.64     8.9544     2.066
     9.84       7.28     9.5630     2000
    14.84       7.30    34.383     6000
    31.01    338.78   3848.03   30707.05
END FTABLE  7

FTABLE      8
rows cols
  4      4
    depth      area      volume      outflow1 ***
      0.        2.51        0.        0.
     0.01       2.51       0.03        0.
     1.16       2.46       2.89       65.36
    25.77    186.12   2992.61  295449.88
END FTABLE  8

```

```

FTABLE          9
rows cols
4      4
      depth      area      volume      outflow1 ***
      0.         5.43       0.         0.
      0.01       5.43       0.05       0.
      1.01       5.31       5.43       44.58
      11.84      132.28     848.34    19856.96
END FTABLE 9
END FTABLES

GENER
OPCODE
#thru# OP- ***
      CODE ***
1      8      10
END OPCODE
PARM
# - # ***      K
1      8      0.91905
END PARM
END GENER

MUTSIN
MUTSINFO
<-range><mfl><npt><nmn><nli><mis> ***
# - # MFL  NPT  NMN  NLI  MSFG ***
01      44    0    09   25    2
02      45    0    09   25    2
03      46    0    09   25    2
20      60    0    08   25    2
END MUTSINFO
END MUTSIN

PLTGEN
PLOTINFO
# - # FILE  NPT  NMN  LABL  PYR  PIVL *** -1=monthly; -2=annual;
1      40    0    8    0    12   24
2      41    0    8    0    12   24
3      42    0    8    0    12   24
END PLOTINFO

GEN-LABELS
# - #<-----Title-----> *** <-----Y axis-
----->
1      Daily Average E.coli      #/100mL
2      Daily Maximum E.coli      #/100mL
3      Daily Minimum E.coli      #/100mL
END GEN-LABELS

SCALING
# - #      YMIN      YMAX      IVLIN      THRESH ***
1      3      0.      1.E+10     100.
END SCALING

```

```

CURV-DATA          (First curve)
      <-Curve label--> Line Intg  Col Tran ***
      # - #          type  eqv  code code ***
      1      R1.EC(livestock)    0    0    1 AVER
      2      R1.EC(livestock)    0    0    1 MAX
      3      R1.EC(livestock)    0    0    1 MIN
END CURV-DATA
CURV-DATA          (Second curve)
      <-Curve label--> Line Intg  Col Tran ***
      # - #          type  eqv  code code ***
      1      R1.EC(pet)          0    0    1 AVER
      2      R1.EC(pet)          0    0    1 MAX
      3      R1.EC(pet)          0    0    1 MIN
END CURV-DATA
CURV-DATA          (Second curve)
      <-Curve label--> Line Intg  Col Tran ***
      # - #          type  eqv  code code ***
      1      R1.EC(septic)       0    0    1 AVER
      2      R1.EC(septic)       0    0    1 MAX
      3      R1.EC(septic)       0    0    1 MIN
END CURV-DATA
CURV-DATA          (Second curve)
      <-Curve label--> Line Intg  Col Tran ***
      # - #          type  eqv  code code ***
      1      R1.EC(wildlife)     0    0    1 AVER
      2      R1.EC(wildlife)     0    0    1 MAX
      3      R1.EC(wildlife)     0    0    1 MIN
END CURV-DATA
CURV-DATA          (Second curve)
      <-Curve label--> Line Intg  Col Tran ***
      # - #          type  eqv  code code ***
      1      R5.EC(livestock)    0    0    1 AVER
      2      R5.EC(livestock)    0    0    1 MAX
      3      R5.EC(livestock)    0    0    1 MIN
END CURV-DATA
CURV-DATA          (Second curve)
      <-Curve label--> Line Intg  Col Tran ***
      # - #          type  eqv  code code ***
      1      R5.EC(pet)          0    0    1 AVER
      2      R5.EC(pet)          0    0    1 MAX
      3      R5.EC(pet)          0    0    1 MIN
END CURV-DATA
CURV-DATA          (Second curve)
      <-Curve label--> Line Intg  Col Tran ***
      # - #          type  eqv  code code ***
      1      R5.EC(septic)       0    0    1 AVER
      2      R5.EC(septic)       0    0    1 MAX
      3      R5.EC(septic)       0    0    1 MIN
END CURV-DATA
CURV-DATA          (Second curve)
      <-Curve label--> Line Intg  Col Tran ***
      # - #          type  eqv  code code ***

```

```

1          R5.EC(wildlife)      0    0    1 AVER
2          R5.EC(wildlife)      0    0    1 MAX
3          R5.EC(wildlife)      0    0    1 MIN
END CURV-DATA
END PLTGEN

NETWORK
<svol><o#> <sgrp> <smem><m#><-mfact--><tr> <tvoll>< range> <tgrp>
<tmem><m#> ***
<-Volume-> <-Grp> <-Member-><--Mult-->Tran <-Target vols> <-Grp> <-
Member-> ***
<Name>    #          <Name> # #<-factor->strg <Name>    #    #          <Name> #
# ***
*** Direct deposits (repeat each data line for each subwatershed)
*** Cattle
MUTSIN 01 OUTPUT      01      1      SAME RCHRES 01      INFLOW IDQAL 1
MUTSIN 01 OUTPUT      02      1      SAME RCHRES 02      INFLOW IDQAL 1
MUTSIN 01 OUTPUT      03      1      SAME RCHRES 03      INFLOW IDQAL 1
MUTSIN 01 OUTPUT      04      1      SAME RCHRES 04      INFLOW IDQAL 1
MUTSIN 01 OUTPUT      05      1      SAME RCHRES 05      INFLOW IDQAL 1
MUTSIN 01 OUTPUT      06      1      SAME RCHRES 06      INFLOW IDQAL 1
MUTSIN 01 OUTPUT      07      1      SAME RCHRES 07      INFLOW IDQAL 1
MUTSIN 01 OUTPUT      08      1      SAME RCHRES 08      INFLOW IDQAL 1
MUTSIN 01 OUTPUT      09      1      SAME RCHRES 09      INFLOW IDQAL 1
*** Wildlife
MUTSIN 02 OUTPUT      01      1      SAME RCHRES 01      INFLOW IDQAL 4
MUTSIN 02 OUTPUT      02      1      SAME RCHRES 02      INFLOW IDQAL 4
MUTSIN 02 OUTPUT      03      1      SAME RCHRES 03      INFLOW IDQAL 4
MUTSIN 02 OUTPUT      04      1      SAME RCHRES 04      INFLOW IDQAL 4
MUTSIN 02 OUTPUT      05      1      SAME RCHRES 05      INFLOW IDQAL 4
MUTSIN 02 OUTPUT      06      1      SAME RCHRES 06      INFLOW IDQAL 4
MUTSIN 02 OUTPUT      07      1      SAME RCHRES 07      INFLOW IDQAL 4
MUTSIN 02 OUTPUT      08      1      SAME RCHRES 08      INFLOW IDQAL 4
MUTSIN 02 OUTPUT      09      1      SAME RCHRES 09      INFLOW IDQAL 4
*** Straight Pipes
MUTSIN 03 OUTPUT      01      1      SAME RCHRES 01      INFLOW IDQAL 3
MUTSIN 03 OUTPUT      02      1      SAME RCHRES 02      INFLOW IDQAL 3
MUTSIN 03 OUTPUT      03      1      SAME RCHRES 03      INFLOW IDQAL 3
MUTSIN 03 OUTPUT      04      1      SAME RCHRES 04      INFLOW IDQAL 3
MUTSIN 03 OUTPUT      05      1      SAME RCHRES 05      INFLOW IDQAL 3
MUTSIN 03 OUTPUT      06      1      SAME RCHRES 06      INFLOW IDQAL 3
MUTSIN 03 OUTPUT      07      1      SAME RCHRES 07      INFLOW IDQAL 3
MUTSIN 03 OUTPUT      08      1      SAME RCHRES 08      INFLOW IDQAL 3
MUTSIN 03 OUTPUT      09      1      SAME RCHRES 09      INFLOW IDQAL 3
*** PreP Spills into Reaches
MUTSIN 20 OUTPUT      01      1      SAME RCHRES 05      INFLOW IVOL
MUTSIN 20 OUTPUT      02      1      SAME RCHRES 05      INFLOW IDQAL 3
MUTSIN 20 OUTPUT      03      1      SAME RCHRES 07      INFLOW IVOL
MUTSIN 20 OUTPUT      04      1      SAME RCHRES 07      INFLOW IDQAL 3
MUTSIN 20 OUTPUT      05      1      SAME RCHRES 08      INFLOW IVOL
MUTSIN 20 OUTPUT      06      1      SAME RCHRES 08      INFLOW IDQAL 3
MUTSIN 20 OUTPUT      07      1      SAME RCHRES 09      INFLOW IVOL
MUTSIN 20 OUTPUT      08      1      SAME RCHRES 09      INFLOW IDQAL 3

```

*** create E. coli timeseries using FC-EC translator equation
 $EC = (FC^{0.91905}) \times 0.98814866$ for RCHRES #1 and #5

*** Livestock; pet; septic

RCHRES	1	GQUAL	DQAL	1	GENER	1	INPUT
RCHRES	1	GQUAL	DQAL	2	GENER	2	INPUT
RCHRES	1	GQUAL	DQAL	3	GENER	3	INPUT
RCHRES	1	GQUAL	DQAL	4	GENER	4	INPUT
RCHRES	5	GQUAL	DQAL	1	GENER	5	INPUT
RCHRES	5	GQUAL	DQAL	2	GENER	6	INPUT
RCHRES	5	GQUAL	DQAL	3	GENER	7	INPUT
RCHRES	5	GQUAL	DQAL	4	GENER	8	INPUT

GENER	1	OUTPUT	0.98814866	PLTGEN	1	INPUT	MEAN	1
GENER	2	OUTPUT	0.98814866	PLTGEN	1	INPUT	MEAN	2
GENER	3	OUTPUT	0.98814866	PLTGEN	1	INPUT	MEAN	3
GENER	4	OUTPUT	0.98814866	PLTGEN	1	INPUT	MEAN	4
GENER	5	OUTPUT	0.98814866	PLTGEN	1	INPUT	MEAN	5
GENER	6	OUTPUT	0.98814866	PLTGEN	1	INPUT	MEAN	6
GENER	7	OUTPUT	0.98814866	PLTGEN	1	INPUT	MEAN	7
GENER	8	OUTPUT	0.98814866	PLTGEN	1	INPUT	MEAN	8

GENER	1	OUTPUT	0.98814866	PLTGEN	2	INPUT	MEAN	1
GENER	2	OUTPUT	0.98814866	PLTGEN	2	INPUT	MEAN	2
GENER	3	OUTPUT	0.98814866	PLTGEN	2	INPUT	MEAN	3
GENER	4	OUTPUT	0.98814866	PLTGEN	2	INPUT	MEAN	4
GENER	5	OUTPUT	0.98814866	PLTGEN	2	INPUT	MEAN	5
GENER	6	OUTPUT	0.98814866	PLTGEN	2	INPUT	MEAN	6
GENER	7	OUTPUT	0.98814866	PLTGEN	2	INPUT	MEAN	7
GENER	8	OUTPUT	0.98814866	PLTGEN	2	INPUT	MEAN	8

GENER	1	OUTPUT	0.98814866	PLTGEN	3	INPUT	MEAN	1
GENER	2	OUTPUT	0.98814866	PLTGEN	3	INPUT	MEAN	2
GENER	3	OUTPUT	0.98814866	PLTGEN	3	INPUT	MEAN	3
GENER	4	OUTPUT	0.98814866	PLTGEN	3	INPUT	MEAN	4
GENER	5	OUTPUT	0.98814866	PLTGEN	3	INPUT	MEAN	5
GENER	6	OUTPUT	0.98814866	PLTGEN	3	INPUT	MEAN	6
GENER	7	OUTPUT	0.98814866	PLTGEN	3	INPUT	MEAN	7
GENER	8	OUTPUT	0.98814866	PLTGEN	3	INPUT	MEAN	8

END NETWORK

EXT SOURCES

WDM3	11	PREC	ENGLZERO	SAME	PERLND	101	607	EXTNL	PREC
WDM2	13	ATEM	ENGL	SAME	PERLND	101	607	EXTNL	GATMP
WDM2	17	DEWP	ENGL	SAME	PERLND	101	607	EXTNL	DTMPG
WDM2	14	WIND	ENGL	SAME	PERLND	101	607	EXTNL	WINMOV
WDM2	15	SOLR	ENGL	SAME	PERLND	101	607	EXTNL	SOLRAD
WDM2	16	PEVT	ENGL	SAME	PERLND	101	607	EXTNL	PETINP
WDM3	11	PREC	ENGLZERO	SAME	IMPLND	101		EXTNL	PREC
WDM2	13	ATEM	ENGL	SAME	IMPLND	101		EXTNL	GATMP
WDM2	17	DEWP	ENGL	SAME	IMPLND	101		EXTNL	DTMPG
WDM2	14	WIND	ENGL	SAME	IMPLND	101		EXTNL	WINMOV
WDM2	15	SOLR	ENGL	SAME	IMPLND	101		EXTNL	SOLRAD
WDM2	16	PEVT	ENGL	SAME	IMPLND	101		EXTNL	PETINP
WDM3	11	PREC	ENGLZERO	SAME	RCHRES	1	9	EXTNL	PREC

WDM2	13	ATEM	ENGL	SAME	RCHRES	1	9	EXTNL	GATMP
WDM2	17	DEWP	ENGL	SAME	RCHRES	1	9	EXTNL	DEWTMP
WDM2	14	WIND	ENGL	SAME	RCHRES	1	9	EXTNL	WIND
WDM2	15	SOLR	ENGL	SAME	RCHRES	1	9	EXTNL	SOLRAD
WDM2	18	CLOU	ENGL	SAME	RCHRES	1	9	EXTNL	CLOUD
WDM2	12	EVAP	ENGL	SAME	RCHRES	1	9	EXTNL	POTEV

END EXT SOURCES

SCHEMATIC

PERLND	101	806.55	RCHRES	1	2
PERLND	201	113.73	RCHRES	1	2
PERLND	301	447.2	RCHRES	1	2
PERLND	401	266.02	RCHRES	1	2
PERLND	102	1136.15	RCHRES	2	2
PERLND	202	29.37	RCHRES	2	2
PERLND	302	125.28	RCHRES	2	2
PERLND	402	95.67	RCHRES	2	2
PERLND	103	280.88	RCHRES	3	2
PERLND	203	39.29	RCHRES	3	2
PERLND	303	325.81	RCHRES	3	2
PERLND	403	247.12	RCHRES	3	2
PERLND	104	10.95	RCHRES	4	2
PERLND	204	35.7	RCHRES	4	2
PERLND	304	95.92	RCHRES	4	2
PERLND	404	51.4	RCHRES	4	2
PERLND	105	50.5	RCHRES	5	2
PERLND	205	23.72	RCHRES	5	2
PERLND	305	290.17	RCHRES	5	2
PERLND	405	534.23	RCHRES	5	2
PERLND	106	3.54	RCHRES	6	2
PERLND	206	33.63	RCHRES	6	2
PERLND	306	24.01	RCHRES	6	2
PERLND	406	197.27	RCHRES	6	2
PERLND	407	139.63	RCHRES	7	2
PERLND	607	6.86	RCHRES	7	2
PERLND	108	57.21	RCHRES	8	2
PERLND	308	77.28	RCHRES	8	2
PERLND	408	698.21	RCHRES	8	2
PERLND	109	3.71	RCHRES	9	2
PERLND	309	6.37	RCHRES	9	2
PERLND	409	491.81	RCHRES	9	2
IMPLND	101	98.63	RCHRES	1	1
IMPLND	101	27.88	RCHRES	2	1
IMPLND	101	78.69	RCHRES	3	1
IMPLND	101	18.77	RCHRES	4	1
IMPLND	101	351.80	RCHRES	5	1
IMPLND	101	72.96	RCHRES	6	1
IMPLND	101	51.64	RCHRES	7	1
IMPLND	101	258.24	RCHRES	8	1
IMPLND	101	181.90	RCHRES	9	1

*** Reach Connections

RCHRES	2		RCHRES	1	3
--------	---	--	--------	---	---

RCHRES 3
RCHRES 4
RCHRES 5
RCHRES 6
RCHRES 7
RCHRES 8
RCHRES 9
END SCHEMATIC

RCHRES 2 3
RCHRES 3 3
RCHRES 4 3
RCHRES 5 3
RCHRES 6 3
RCHRES 7 3
RCHRES 7 3

MASS-LINK

MASS-LINK 2
<-Volume-> <-Grp> <-Member-><--Mult-->
Member-> ***
<Name> <Name> x x<-factor->
x ***
PERLND PWATER PERO 0.0833333
PERLND SEDMNT SOSED 1 0.05
PERLND SEDMNT SOSED 1 0.60
PERLND SEDMNT SOSED 1 0.35
PERLND PQUAL POQUAL 1 1.00
PERLND PQUAL POQUAL 2 1.00
PERLND PQUAL POQUAL 3 1.00
PERLND PQUAL POQUAL 4 1.00

END MASS-LINK 2

MASS-LINK 1
IMPLND IWATER SURO 0.0833333
IMPLND SOLIDS SOSLD 1 0.10
IMPLND SOLIDS SOSLD 1 0.50
IMPLND SOLIDS SOSLD 1 0.40
IMPLND IQUAL SOQUAL 1 0.00

END MASS-LINK 1

MASS-LINK 3
RCHRES ROFLOW
END MASS-LINK 3

MASS-LINK 4
RCHRES ROFLOW ROVOL
RCHRES HYDR RO
END MASS-LINK 4

MASS-LINK 5
RCHRES OFLOW 1
END MASS-LINK 5

MASS-LINK 6
RCHRES OFLOW 2
END MASS-LINK 6
END MASS-LINK

END RUN

<-Target vols> <-Grp> <-
<Name> <Name> x
RCHRES INFLOW IVOL
RCHRES INFLOW ISED 1
RCHRES INFLOW ISED 2
RCHRES INFLOW ISED 3
RCHRES INFLOW IDQAL 1
RCHRES INFLOW IDQAL 2
RCHRES INFLOW IDQAL 3
RCHRES INFLOW IDQAL 4

RCHRES INFLOW IVOL
RCHRES INFLOW ISED 1
RCHRES INFLOW ISED 2
RCHRES INFLOW ISED 3
RCHRES INFLOW IDQAL 1

RCHRES INFLOW

COPY INPUT MEAN 1
COPY INPUT MEAN 2

RCHRES INFLOW

RCHRES INFLOW